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OM nucleic - nucleic search, using sw model

Run on:

July 18, 2003, 19:01:57; Search time 4798 Seconds (without alignments) 11239.579 Million cell updates/sec

US-09-977-221-2-C-AI-1513 1853 1 aaaacgcagggagggaggct......cgtctgtaatcccaccttt 1853 Title: Perfect score:

Sequence:

Scoring table: IDENTITY\_NUC Gapext 1.0

2054640 segs, 14551402878 residues

Searched:

4109280 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database :

11. 95 ba: \*
22. 92 bht: \*
43. 95 bn: \*
55. 95 bv: \*
77. 95 pat: \*
77. 95 pat: \*
10. 95 pr: \*
11. 95 sts: \* em\_fun:\* em\_hum:\* gb\_sy:\* gb\_un:\* gb\_vi:\* em\_ba:\* em\_mu:\* em\_in:\* em\_or:\* em\_ov:\* em\_om:

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

- 4 00 00 00 00 00 00 00 00 00 00 00 00 0	X93505 AR086632 AR134626 AR134620 U47031 U32497 V18008 G AF000038 AF308149 AF308149
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ALIGNMENTS

PAT 20-JUN-2002 Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. linear DNA Morten,J.E. Polymorphisms in the human p2x7 gene Patent: #FP 1199372-A 2 24-APR-2002; AX427649 1853 bp Sequence 2 from Patent EP1199372. AX427649 AX427549.1 GI:21537769 human. RESULT 1
AX427649
LOCUS
DEFINITION
ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL

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1381 TTCCTGGACAACCAGAGGAGATACAGCTGCTTAGAAAGGAGGCGACTCCTAGATCCAGGG 1440
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Buell, G.N.
Direct Submission
Submitted (21-NOV-1996) G.N. Buell, Geneva Biomedical Research
Institute, Molecular Biology, 14 chemin des Aulx, 1228
Plan-les-Ouates, Geneva, SWITZERILAND
Location/Qualifiers
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/protein_id="CAA70755.1"
/db_xref="GI:1854512"
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361 AAGGCCAAGAGCAGCGGTTGTGCCCCAGTATCCCACCGCAGGAGGCTCTGTTCCTCTG 420	421 ACCGAGGTTGTAAAAGGGATGGATGGACCCGCAGAGCAAAGGAATTCAGACCGGAAGGT 480	481 GIGPACTRYANGAAGGGAACCAGAAGCCTGTGAAGTCTCTGCCTGGTGCCCCATCGAGG 540	541 CAGTGGAAGGCCCCCCGGCCTGCTCTTGAACAGTGCCGAAAACTTCACTGTGCTCA 600 	601 TCAAGAACAATATCGACTTCCCCGGCCAACTACACCAGGAAAACATCCTGCCAGGTT 660 	661 TAAACATCACTTGTACCTTCCAGAAGACTCGAGAGTCCACAGTGTCCCATTTTCCGACTAG 720 	721 GAGACATCTTCCGAGAAACAGGCGATAATTTTTCAGATGKGGCAATTCAGGGCGGAATAA 780 	781 IGGCCATTGACATCTACTGGCACTGCAACCCTAGATTCCATCACTGCCRTCCCA 840	841 AATACAGTTTCCRTCGCCTTGACGACAAGACCACCAAGGTGTCCTTGTACCCTGGCTACA 900 	901 ACTTCAGATACGCCAAGTACTACAAGGAAAACAATGTTGAGAAACGGACTCTGATAAAAG 960 	961 TCTFCGGGATCCGTTFTGACATCCTGGFTFTTGGCACGGGGGAAAATTTGACATTATCC 1020 	1021 AGCIGGTIGIGIACAICGGCTCAACCCTCICCTACTICGGCCTGGCCRCIGITCATCG 1080	1081 ACTTCCTCAFCGACASTTACTCCAGTAACTGCTCGCTCCCATATTTATCCCTGGTGCA 1140	AGTGCTGTCAGCCCTGTGTGGTCAACGAATACTACTACAGGAAGAAGTGCGAGTCCATTG	1201 TGGAGCCAPAGCCGACATTAPAGTATGTGTCCTTTGTGGATGAATCCATTAGGATGG 1260	1261 TGAACCAGCAGCTACTAGGGAGAAGTCTGCAAGATGTCAAGGGCCAAGAAGTCCSAAGAC 1320 	1321 CTGFGATGGACTTCACAGATTGTCCAGGCTGCCCCTGGCCGTCCATGACACCACCCCGA 1380	1381 ITCCTGGACAACCAGAGATACRGCTGCTTAQAAAGGAGGCGACTCCTAGATCCAGGG 1440	1441 ATAGCCCYGTCTGGTGCCAGTGTGGAAGCTGCCTCCCATCTCCAACTCCCTGAGRGCCACA 1500
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1501 GGTGCCTGGAGGCGCTGTGCTGCCGGAAAAAGCCGGGGGCCTGCATCACCACCTCAGAGC 1560 	1561 TGTTCAGGAAGCTGGTCCTGTCCAGACACGTCCTGCAGTTCCTCCTGCTCTACCAGGAGC 1620	1621 CCTTGCTKGCGCTGGATTGGATTCCACCAACAGCCGGCTGCGGACTGTGCCTACAGGT 1680	1681 GCTACGCCACCTGGCGCTTCGGCTCCCAGGACATGGCTGACTTTGCCATCCTGCCCAGCT 1740	1741 GCTGCCGCTGGAGGATCCGGAAAGAGTTTCCRAAGAGTGAAGGGCAGTACAGTGGCTTCA 1800 	1801 AGAGTCCTTACTGAAGCCAGGCACCGTGGCTCACGTCTGTAAFCCCACCTTT 1853	T 3 693 1052 1052 1052 1053 1053 1053 1053 1053 1053 1053 1053	ANILOGOS 19 from patent US 6133434. SION ARI16693 GI:14097015	Σ	E 1 (bases 1 to 1853) S Buell,G.Nutter., Surprenant Purinergic receptor L Patent: US 6133434-A 19.17-1	FENTURES LOCATED LOCATION FER SOURCE 11853 (Arganism="unknown" 1855 a 503 c 477 g 418 t ONIGIN	Query Match 99.5%; Score 1843.8; DB 6; Length 1853; Best Local Similarity 99.1%; Pred. No. 0; Matches 1836; Conservative 15: Mismatches 2; Indels 0; Gaps 0;	GGAGGGAGGCTGTCACCATGCCGCCTGCTGCAGCTGCAGTGATGTTTCC 60 GGAGGGAGCTGTTACCATGCCGCCTGCTGCAGCTGCAGTGATGTTTCC 60 GGAGGAGGCTGTCACCATGCCGCTGCTGCAGTGAATGTTTTCC 60	AGTATGAGACGAACAAGTCACTGGGATCCAGAGCATGAATTATGGCACCATTAAGTGGT 1	TCTTCCACGTGATCATCTTTCCTACGTTTGCTTTGCTCTGGTGAGTGA	AGGGAAAGAGCCTGTCATCCTAGTTTGCTTTGCTCTGGTGTGTGT	ANGRAGARARAKAN TARAKARAN TARAKARAKARAN TARAKARAN TARAKAR	ACTACACCTTCCCTTTGCAGGGAACTCTTCTCGTGATGACAACTTTCTCAAAACG	301 ACTACACCTTCCCTTTGCAGGGAACTCTTTCGTGATGACAAACTTTCTCAAAACAG 360
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/translation="MPACCSCSDVFQYETHKUTRIQSMNYGTIKWFFHVIIFSYVCFA
IVSDKLYQRKEPVISSVHTKVKGIAEVKEEIVENGVKKLVHSVEDTADYTFFLQGNSF
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TCEVSAMCEIRAVEEAPPRALMSAENFTVLIKNHIDFGHNYTTRHILDFGLNITCTF
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TSELFRKIVLSRHVLQFLLLIKQBFLALDVDSTNSRIRHCAYRCYATWRFGSQDMADF
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                                                                         /tissue_type="Skin, melanotic melanoma, high MDR./clone_lib="NIH_MGC_49"
/lab_host="DH10B-R"
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Context.
Sheychenko,Y., Wetherby.K.D., Beckstrom-sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J. Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,W., Maduro,Q.L., Masilello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
1561 TGTTCAGGAAGCTGGTCCTGTCCAGACACGTCCTGCAGTTCCTCCTGCTCTACCAGGAGC 1620
                                                                                                                                                                                                                                                                                        GGTGCCTGGAGGCGCTGTGCTGCCGGAAAAAGCCGGGGGCCTGCATCACCACCTCAGAGC 1560
                                                                                                                      1501 GGTGCCTGGAGGAGCTGTGCTGCCGGAAAAGCCGGGGGCCTGCATCACCACCTCAGAGC 1560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens, Similar to purinergic receptor P2X, ligand-gated ion channel, 7, clone MGC:20089 INAGE:4298811, mRNA, complete cds. BC011913. GI:15080308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (30-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                      1561 TGTTCAGGAAGCTGGTCCTGTCCAGACACGTCCTGCAGTTCCTCCTGCTCTACCAGGAGC
                                                                                                                                                                                                                                                               CCTTGCTKGCGCTGGATGTGGATTCCAACAACAGCCGGCTGCGGGCACTGTGCCTACAGGT
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Contact: MGC help desk
Emal: cgapbe-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gailbersburg, Maryland:
Web site: http://www.nisc.nih.gov/
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Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates;
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KEYWORDS SOURCE ORGANISM

TITLE JOURNAL

REFERENCE AUTHORS

DEFINITION

RESULT 4 BC011913

ACCESSION

VERSION

source

FEATURES

QY Db

1426	PRESULT 8  TANDZYGEN  LOCUS  LOCUS  LOCUS  R. HORVEGICUS MRNA for ATP ligand gated ion channel.  ACCESIAN X9582.  VERSION  RATUS  RATUS  RATUS  RATUS  RATUS  RATUS  REPERBNCE  VERSION  REPERBNCE  VERSION  REPERBNCE  VERSION  REPERBNCE  VERSION  REPERBNCE  VERSION  NAUTHORS  LOAD  JOURNAL  Science 272  Casto  JOURNAL  Science 272  Casto  JOURNAL  Science  Load  JOURNAL  Science  JOURNAL  Science  JOURNAL  Science  JOURNAL  Science  JOURNAL  JOURNAL  Load  JOURNAL  JOURNAL  Load  JOURNAL  JOURNA
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                                                CGCCAAGTACTACAAGGAAAACAATGTTGAGAAACGGACTCTGATAAAAGTCTTCGGGAT
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/translation="MPACCSWNDVFQYETNKVTRIQSVNYGTIKWILHMTVFSYVSFA
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TCEIFRWCPAEBEGKEAPFRALLRSAENFTVLIKNNIDFPGHNYTTRNILLPGNNISCTF
HTWNPROPETRICISIFQETGENTFTANTANGGLIMGETTWOCKNEY
RLDDKTYNNESIFPOTHEKATYKENNMEKRTIKAFGYRFDILLYGGTGGKFDIIOLV
VYIGSTLSYFGLATVCIDLINTYASTCCRSRVYPSCKCEPCANNEYTYRKCEPIV
ENFTLKKYSVEDEPHIMVOQQLIAGRADDYNOCGHCLFSGLEHGHSP
PIFGQPPEMQLLQIFAGRADDSGARGDNOCGHCLPSOLPERGERGELEHGHSP
TSELFSKIVLSREALQLLLLLYGBPLLALEGGENINSKLREELCCRRKFGGOTT
TSELFSKIVLSREALQLLLLLEGGENINSKLRRCHRCARRSATWRFVSQDMADF
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     AACCTAGACCGTTGGTTCCATCACTGCCRTCCCAAATACAGTTTCCRTCGCCTTGACGAC
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                                                                                                            CICITGAACAGTGCCGAAAACTICACTGTGCTCATCAAGAACAATATCGACTTCCCCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCCAGAGCACGAATTATGGCACCGTCAAGTGGGTCTTGCACATGATCGTCTTTTCCTAC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98
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                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                           Simon, J.

Direct Submission

Direct Submission

Submitted (28-JUL-1998) Simon J., Department of Pharmacology,
Submitted (28-JUL-1998) Simon J., Department of Pharmacology,
University of Cambridge, Glaxo Institute of Applied Pharmacology,
Tennis Court Road, Cambridge, CB2 107, UNITED KINGDOM

(Chassell, I.P., Simon, J., Hibell, A.D., Michel, A.D., Barnard, E.A. a

Rumphrey, P.P.A.

Cloning and Functional characterisation of the mouse P2X7 receptor

FEBS Lett. 4390, 260-300 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTTGCTTTGCTCTGGTGAGTGACAAGCTGTACCAGCGGAAAGAGCCTGTCATCAGTTCT
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                             ROD
                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
          Mus musculus mRNA for P2X7 receptor subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="ATP gated ion channel"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="MTW8"
/cell_type="microglia"
/note="immortalised cell line"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AILPSCCRWRIRKEFPKTEGQYSGFKYPY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1269.6;
Pred. No. 0;
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403 t
                                                                                                                         P2X7 gene; P2X7 receptor subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=experimental
                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
1 (bases 1 to 1810)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="P2X7"
12. .1799
                                                                                                 AJ009823.1 GI:4007637
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ilarity 81.3%;
Conservative 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="P2X7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         490
                                                                                                                                                                                 Mus musculus
                                                                                                                                                      house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87
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ORIGIN
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NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                              Center project Information
Center project name: 12887
Center clone name: 6_F_188
Center clone name: 6_F_1887
Center clone name: 6_F_1887
Center clone project name: 12887
Sequencing vector: M13; M7815; 100% of reads
Chamistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 160480 bases at least Q40
Consensus quality: 165583 bases at least Q30
Consensus quality: 165583 bases at least Q30
Insert size: 182000; agarose-fp
Insert size: 189065; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
          Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 bp
of 2276 bp in length
100 bp
of 2642 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48925: gap of 100 bp 56101: contig of 7176 bp in length 56201: gap of 100 bp 68011: contig of 11810 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120698 120797: gap of 100 bp
120798 143533: contig of 22736 bp in length
145534 143633: gap of 100 bp
143634 171065: contig of 27432 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78044: gap of 100 bp
90143: contig of 12099 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104983 105082: gap of 100 bp
105083 120697: contig of 15615 bp in length
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104982: contig of 14739 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 1071: contig of 1071 bp in length
1072 1171: gap of 100 bp
1072 2771: contig of 1000 bp in length
2172 2271: gap of 100 bp
2272 3677: contig of 1406 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17524; gap of 100 bp 21923: contig of 4399 bp in length 22023; gap of 100 bp 25017: contig of 2994 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29337: gap of 100 bp 34192: contig of 4855 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34193 34292; gap of 100 bp 43423 44041: contig of 6179 bp in length 40472 40571; gap of 100 bp 40572 48825; contig of 6254 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 bp
of 1406 bp in length
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of 4278 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25117: gap of 100 bp
29237: contig of 4120 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77944: contig of 9833 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-6F18"
/clone_lib="RPCI-11 Human Wale BAC"
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/note="assembly_fragment"
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3678 3777; gap of 10
3778 6053; contig of
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6154 8795; cont
8796 8895; gap of
8896 13173; cont
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68112 77944: cont
77945 78044: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17524: gap of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it
be preserved.
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25118
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Shiren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Balawin, J., Barna, M., Beckerly, R., Boguslay'ry, L., Boukhgalter, B., Brown, A., Castle, A., Collins, S., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, K., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehocky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McDwan, P., McGurk, A., McErnan, K., McLaughlin, J., Meltin, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wan, X., Wann, D., Few, J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Winnell, A., Wassiliev, H., Vo, A., Wheeler, J., Wu, X., Wann, D., Peterson, M., Silmmer, A. and Zody, M., Wille, J., Wu, X., Wann, D., Peterson, M., Silmmer, A. and Zody, M., Walle, J., Wu, X., Wann, D., Peterson, M., Silmmer, A. and Zody, M., Wille, J., Wu, X., Wann, D., Peterson, M., Silmmer, A., and Zody, M., Wille, J., Wu, X., Wann, D., Peterson, M., Silmmer, A., and Zody, M., Walle, J., Wu, X., Wann, M., Walle, M., Walle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC011216 171065 bp DNA linear HTG 26-WAY-2000
HOMO Sapiens clone RP11-6F18, WORKING DRAFT SEQUENCE, 21 unordered
pieces.
                                                                                                                                                                                                                                                                                                                          AAAAAGCCGGGGGCCTGCATCACCACCTCAGAGCTGTTCAGGAAGCTGGTCCTGTCCAGA 1586
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1587 CACGTCCTGCAGTTCCTCCTGCTCTACCAGGAGCCCTTGCTKGCGCTGGATGTGGATTCC 1646
                                                             CIGCITAGAAAGGAGGCGACTCCTAGATCCAGGGATAGCCCYGTCTGGTGCCAGTGTGGA '1466
                                                                                                                                                                                                                                                                                                                                                                                    1512 AGGAAGCCGGGGGGGTGCATCACCACCTCCAAGCTCTTCCATAAGCTCGTGCTGTCCCGA 1571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1392 CTGCTCCATGAAGAGGTGGCCCCTAAGTCCGGGGACAGCCCGAGTTGGTGCCAGTGTGGA 1451
1332 AGGCTGTCCCTATCTCTCCACGACTCACCCCTGACTCCTGGACAATCTGAGGAAATTCAG 1391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                        1452 AATIGCCTCCCGTCTCGCCTACCGGAGCAGCAGGAGCAGCTGTGCTGCCGG
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                                                                                                                                                                                               AGCTGCCTCCCATCTCAACTCCCTGAGRGCCACAGGTGCCTGGAGGCGCTGTGCTGCCGG
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Web site: http://www-seq.wi.mit.edu
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AC011216.4 GI:8072519
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1 (bases 1 to 171065)
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96053 ACCAGGAGCCCTTGCTGGCGCTGGATGTGGATTCCACCAACAGCCGGCTGCGGCACTGTG 95112
                                                                                                                        1312 TCCSAAGACCTGYGAGTGGACTTCACAGATTTGTCCAGGCTGCCCCTGGCCTCCATGACA 1371
                                   1672 CCTACAGGTGCTACGCCACCTGGCGCTTCGGCTCCCAGGACATGGCTGACTTTGCCATCC 1731
                                                                                                      1732 IGCCCAGCTGCTGCTGCTGGAGGATCCGGAAAGAGTTTCCRAAGAGTGAAGGGCAGTACA 1791
                                                                                                                                                                        1792 GTGGCTTCAAGAGTCCTTACTGAAGCCAGGCACGTGGCTCACGTCTGTAATCCCACCTT 1851
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1 (Dass 1 to 6839)
Buell, Talabot, F., Gos, A., Lorenz, J., Lai, E., Morris, M.A. and Antonarakis, S.B.
Gene structure and chromosomal localization of the human P2X7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (29-APR-1997) G.N. Buell, Geneva Biomedical Research
Institute, Molecular Biology, 14 Chemin des Aulx, 1228
Flan-les-Cuates, Geneva, SWITZERLAND
Related sequence: Y09561.
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/clone_11b="Dupont Merck P1 library #1"
/dev_atage="adult"
/1516..5962
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/gene="P2X7"
/mumber=12
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1462 c 1523 g 179
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Y12855
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/gene="P2X7"
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2 (bases 1 to 6839)
Buell,G.N.
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Homo sapiens.
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143634. 171065
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22024. .25017
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/note="assembly_fragment"
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120798. .143533
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Rumanla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 228935)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.D., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Binage,K., Blamed,R., Brown,R., Bonnin,D., Barbaria,J., Benton,J., Binage,K., Blame, M., Brown,R., Barks,T., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,R., Charter,M., Cavazos,S.R., Christopoulos,C., Clereland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delagdo,O., Denn,A.L., Ding,Y., Durbin,R.J., Barnhart,C., Edgar,D., Edwards,C.C., Edgar,D., Edwards,C.C., Edgar,D., Edwards,C.C., Edgar,D., Garcia,A., Garner,T., Garze,P., Frantz,P., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gorrell,J.H., Guevara,W., Gunarahe,P., Haws,A., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Harris,C., Harris,K., Harris,C., Hordy,D., Kovar,C., Kratovic,J., Kratovic,J., Kratovic,J., Kratovic,J., Kratovic,J., Ewils,J., Lewis,L., Lewis,L., Lewis,L., Lewis,L., Lewis,L., C., Lewis,L., C., Lewis,L., Lewi
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Homo sapiens chromosome 12 clone RP11-340F14, WORKING DRAFT
                                                                    1372 CACCCCCATTCCTGGACAACCAGAGGAGATACRGCTGCTTAGAAAGGAGGCGGACTCCTA 1431
                                                                                                         1432 GATCCAGGGATAGCCCYGTCTGGTGCCAGTGTGGAAGCTGCCTCCCATCTCAACTCCCTG 1491
                                                                                                                                                                                                                                                                            5580 GATCCAGGGATAGCCCCCGTCTGGTGCCAGTGTGGAAGATGCCTCCCATCTCAACTCCCTG 5639
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5460 TTCAGAGACCTGCGATGGACTTCACAGATTTGTCCAGGCTGCCCCTGGCCCTCCATGACA 5519
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Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwarl,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., McLeod,M.P., Martindale,A., Martinez,E., Massey,E., McLeod,M.P., Moador,M., Mel,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,N., Nguyen,N., Nadyen,N., Notenson,E., Novenkwo,S., Oguh,M., Okwnonu,G., Oragunye,N., Oyiedo,R., Pace,A., Payton,B., Perery,J., Perer,L., Pickens, P., Pickenson,R., Polocka, P., Pace,A., Pace,A., Payton,B., Perery,J., Perer,L., Sutton,M., Son, Ren,Y., Rives,M., Rojas,A., Paluokan,J., Shen,H., Shooshtari,N., Sison,I., Soherer,S., Soctt,G., Shen,H., Shooshtari,N., Sison,I., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Ward,Norde,S., Warten,R., Washington,C., Walliams,G., Williams,G., Williams,G., Williamson,A., Walliamson,A., Walliamson,A., Walliamson,A., Walliamson,B., Sontilla,S., Nelson,D., Welliams,G., Whilliams,G., Walliamson,A., Zorrilla,S., Nelson,D., Verney, W., Y., Wu,Y., Wu,Y.
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* (see http://www.hgsc.bcm.tnc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* Consists of 7 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Worley, K.C.

Submitted (22-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

(Dasss 1 to 228935)

Norley, K.C.

Direct Submission

Submitted (31-UL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemistry: Dye-primer Bodipy: 18% of reads
Chemistry: Dye-terminator Big Dye: 82% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 227917 bases at least 040
Consensus quality: 228951 bases at least 030
Consensus quality: 228915 bases at least 020
Estimated insert size: 217327; sum-of-contigs estimation
Quality coverage: 11x in 020 bases; sum-of-contigs estimation
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gap of unknown length
contig of 2390 bp in length
gap of unknown length
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Web site: http://www.hgsc.bcm.tmc.edu/
Drafting Center Code: BCM
Contact: hgsc-help@bcm.tmc.edu
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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        Direct Submission
Submitted (0.740G-1998) Veterinary Pathobiology,
Missouri, 201 Connaway Hall, Columbia, MO 65211,
Location/Qualifiers
                                                                                                                       /cell_line="bovine aortic endothelial
1. .>504
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Pred. No. 5e-89;
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Rattus norvegicus clone CH230-83K8,
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                                                                       1. .504
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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29597: contig of 8565 bp in length
29697: gap of unknown length
115777: contig of 86080 bp in length
115877: gap of unknown length
228935: contig of 113058 bp in length.
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MARINDA, Adams, C., Adio-Oddola, B., Ali-Osman, F. R., Allen, C., Amaratunge, H. C., Are, J. R., Ayele, M., Banks, T., Barder, J., Benton, J., Bange, R., Blange, K., Blankenburg, K., Bonnin, D., Barder, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Barder, J., Benton, J., Bange, K., Blankenburg, K., Bonnin, D., Borde, J., Berton, E., Burch, P., Burket, C., Burch, R., Chen, S., Chen,
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NOTE: This is a 'working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (08-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77036, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 56726 bases at least 040 Consensus quality: 55422 bases at least 030 Consensus quality: 61794 bases at least 030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/
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Worley, K.C.
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* This record will be updated with the finished sequence
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Birren, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barnan, N., Basitan, V., Bloom, T., Boguslawikiy, L., Anderson, S., Barnan, N., Basitan, V., Bloom, T., Enguslawikiy, L., Boukhqalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dlaz, J.S., Dodge, S., Faro, S., Ferreita, P., Fitzhigh, M., Gage, D., Galaqan, J., Gardyna, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hards, S., Kanat, A., Karatas, A., Kalls, C., LaRocque, K., Lamazares, R., Kanatas, A., Kalls, C., Larocque, K., Lamazares, R., Mancean, C., Macchan, P., Marguis, N., Matthews, C., Macchan, P., Marguis, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norman, C., H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, R., Santos, R., Sahaer, S., Schwer, S., Schwer, S., Schwer, S., Schwer, S., Schwer, R., Schwer, S., Schwer, R., Schwer, S., Schwer, R., Schwer, R., Stander, S., Theodore, J., Topham, K., Travers, M., Travers, M
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Score 344.4; DB 2; Length 66872;
Pred. No. 4.2e-77;
2; Mismatches 103; Indels 0;
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Matches
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zahnoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                   Submitted (18-WAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 18, 2002 this sequence version replaced gi:20128322.
                                                                                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * sequencing reads that have not been assembled into contigor. Runs of N are used to separate the reads and the order in which they appear is completely * arbitrary. Low pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. * However, it should not be assumed that this clone * will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
                                                                                                                                                                                                                       All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L22320
Center clone name: 37_P-22
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of 690 bp in length
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of 687 bp in length
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1312 TCCSAAGACCTGYGAIGGACTTCACAGATTTGTCCAGGCTGCCCTGGCCCTCCATGACA 1371
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Search completed: July 18, 2003, 22:13:47 Job time : 4809 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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			Description		Human P2X7 gene co	Human P2X 7/P2Z co	Human cDNA clone C	Human secreted pro	Rat P2X_7/P2Z codi	HPURR nucleic acid	Nucleotide sequenc	Human brain P2x-1	Rat superior cervi
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			8	-	24	22	22	13	22	19	22	18	17
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                                                                                        AGTATGAGACGAACAAAGTCACTCGGAICCAGAGCATGAATTATGGCACCATTAAGTGGT 120
                                                                                                   AAGGCCAAGAGCAGCGGTTGTGTCCCGAGTATCCCACCCGCAGGACGCTCTGTTCCTCTG 420
                                                                                                                                                                                                                                                                                                                                                ACCGAGGTTGTAAAAAGGGATGGATGGACCCGCAGAGCAAAGGAATTCAGACCGGAAGGT 480
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                                                              AAAACGCAGGGAGGGAGGCTGTCACCATGCCGGCCTGCTGCAGCTGCAGTGATGTTTTCC
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                                       1 AAAACGCAGGGAGGCTGTCACCATGCCGGCCTGCTGCAGCTGCAGTGATGTTTCC
                Gaps
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                Indels
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   Pred. No. 0;
15; Mismatches
   99,1%;
               Matches 1837; Conservative
     Best Local Similarity
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                                                                                                                      /*tag= i
/note= "Single nucleotide polymorphism"
replace (1315, G)
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/*tag= q
/note= "Single nucleotide polymorphism"
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replace (1448, T)
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                                                                                 /*tag= h
/note= "Single nucleotide replace (1096, G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polymorphisms in the human P2X7 gene, pharmacogenetics analysis and drug design
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                                                            /note= "Single nucleotide
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                                      (853, A)
  (835, A)
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-APR-2001;
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99.6%; Score 1845.4; DB 24; Length 1853;

Query Match

540

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ACCGAGGTTGTAAAAAGGGATGGATGGACCCGCAGAGCAAAGGAATTCAGACCGGAAGGT
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Matches 1836; Conservative
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AGCIGGIIGIGIACAICGGCICAACCCICTCCIACIICGGICIGGCCGCTGIGIICAICG 1080
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                                                                                                                                                                                                                                                                                     AGTGCTGTCAGCCCTGTGTGGTCAACGAATACTACTACAGGAAGAAGTGCGAGTCCATTG
                                                                                                                                      TGAACCAGCAGCAACTAGGGAGAAGTCTGCAAGATGTCAAGGGCCAAGAGTCCCAAGAC
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                       ACTICCICAICGACASTIACTCCAGIAACTGCTGTGCCTCCCAIAITIAICCCTGGTGCA
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The present sequence is the coding sequence for human purinergic receptor P2X_7/P2x. This sequence can be used to treat disorders of the nervous system, particularly diseases with a component of chronic inflammation, such as Alzheimer's disease, diseases involving acute or chronic inflammation such as rheumatoid arthritis, amyloidosis, bacterial, viral and other microbial infections, disorders of the haematopoietic system and immune response such as autoimmune disorders, allergies and impoproliferative disorders, diseases involving apoptotic cell death, such as cardiac and cerebral ischaemia and microbial infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGIATGAGACGAACAAAGICACTCGGATCCAGAGCATGAATTATGGCACCATTAAGIGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                particularly tuberculosis. The human P2X_7 gene has been localised to
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                                                                                                                                                                                       modulators which are useful for treating arthritic, respiratory disorders and neurodegenerative disorders, and to generate receptors
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                                                                                                                                                   useful for screening for
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99.1%; Pred. No. 0;
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                                                                                                                                                   Mammalian purinergic receptor (P2X7)
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1561 TGTTCAGGAAGCTGGTCCTGTCCAGCTCTCTCTCTCTCTC	RESULT 3 AAF98411 ID AAF98411 standard; cDNA; 2168 BP. XX AC AAF98411; XX	,	For insolated nucleic acids encoding polypeptides, useful for modulating PT e.g. cytokine and cell prollferation/differentiation activity, the immune system and hematopoiesis regulating activity - the immune system and hematopoiesis regulating activity - the immune system and hematopoiesis regulating activity - the prevented by the prevented in AAF98489 encode secreted continue AAB90667 - AAB90750. The cDNA clones are isolated from various continue AAB90667 - AAB90750. The cDNA clones are isolated from various continue and and may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression. The colypeptides and nucleic acids may be used as nutrients or to modulate controlly and in modulation of the immune system. The cDNA sequences, convolved in modulation of the immune system. The cDNA sequences, proteins, their agonists and/or antagonists exhibit haematopoiesis controlly indiminatory activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic activity; receptor/ligand activity; anti-inflammatory activity; and/or haematopoiesis activity; calherin/tumour suppressor activity; and/or tumour inhibition activity. Included in the invention are probes
481 GTGTAGTRYATGAAGGGAACCAGAAGACTGTGAAGTCTCTGCTGGTGCCCCATGAGG 540  [	QY         781 TGGGCATTGAGATCTACTGGGACTGCAACCTAGATCGATC	QY         1021 AGCTGGTTGTACATCGGCTCAACCCTCCTACTTCGGCCRCTGTTCATCG 1080           DD         1021 AGCTGTTGTGTACATCGGCTCACCTCCTCCGCCGCCGTTCATCG 1080           DD         1081 ACTTCCTCATCGACACTCTCCTCCTCCTCCCTCCTCTCTTCGTGCT 1140           DD         1081 ACTTCCTCATCGACACTTACTCCAGTACTTTATCCTGGTGCA 1140           DD         1081 ACTTCCTCATCGACACTTACTCCAGTACTGCTGCTCCCTTATTTAT	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This cDNA clone, designated CO390_1, codes for a novel human secreted protein (see AAW5830). It was isolated from a human adult brain cDNA library using methods selective for CDNSa that encode secreted proteins. The clone is deposited in composite clone factors and contain an oligonucleotide (see AAT99732) has been designed to isolate CO390_1 DNA from the composite clone. The nucleotide sequence may contain an Alu repetitive element. Novel cDNA clones sequence may contain an Alu repetitive element. Novel cDNA clones can claimed. These can be used for recombinant production of the secreted proteins for analysis, characterisation, diagnostic or harpourie use. They can also be used as tissue or mol. wt. markers, for chromosome identification, to identify genetic disorders, to generate continuous may have many biological activities. For cytckine, immunomodulator, chematopolesis regulating activity, tissue growth activity, activin contains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              haemostatic and thrombolytic activity, receptor/ligand activity, antiinflammatory, cadherin and tumour invasion suppressor activity, and tumour inhibition activity. The proteins can be expressed in vivo from DNA, introduced in gene therapy vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding secreted protein from human cells - useful, e.g. as immunomodulator, antitumour agent, promoters of tissue growth, haemostatic and thrombolytic agents etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19; Length 2169;
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                                                                                                                                                                                                                                                                                                                                                          McCoy JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.9%; Score 1832.2;
98.4%; Pred. No. 0;
ive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                          ER,
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                                    Location/Qualifiers
87..1874
/*tag= a
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Treacy M;
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Matches 1819; Conservative
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                                                                                                                                                                                                                                                                                                                                                          J, Jacobs 1
Spaulding 1
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P-PSDB; AAW58390.
Homo sapiens
                                                                                                                         W09817687-A2
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                                                                                                                                                                                                                                                  24-OCT-1997;
                                                                                                                                                                                                                                                                       25-OCT-1996;
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                                                                                                                                                                  30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                             Racie LA,
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                                                                                                 The present sequence is the coding sequence for rat purinergic receptor P2X_7/P2Z. This sequence can be used to treat disorders of the nervous system, particularly diseases with a component of chronic inflammation, such as Alzheimer's diseases, diseases involving acute or chronic inflammation such as rheumatoid arthritis, amyloidosis, bacterial, viral and other microbial infections, disorders of the hematopolatic system and immune response such as autoimmune disorders, allergies and lymphoproliferative disorders, diseases involving apoptotic cell death, such as cardiac and cerebral ischaemia and microbial infections,
                                                                                                                                                                                                                                                                                                                                                                                                          70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAGTGGTTCTTCCACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATCATCITITCCTACGTTTGCTTTGCTCTGGTGAGTGACAAGCTGTACCAGCGGAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAAGGGAACCAGAAGACCTGTGAAGTCTCTGCCTGGTGCCCCATCGAGGCAGTGGAAGA
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                  to generate receptors
                                                                                                                                                                                                                                                                                                                                    Length 3540;
 treating arthritic, respiratory
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                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                       324;
              disorders and neurodegenerative disorders, and specific antibodies -
                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0;
1; Mismatches
                                                                                                                                                                                                                                                                                                   Sequence 3540 BP; 919 A; 958 C; 899 G; 764
                                                                                                                                                                                                                                                                                                                                    Score 1281.2;
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                                                                      English.
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81.4%;
useful
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                                                                                                                                                                                                                                                                                                                                                                          Conservative
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 modulators which
                                                                      Fig 1B;
                                                                                                                                                                                                                                                                                                                                                                          Matches 1469;
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                                                                      Claim 3;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarthritic; antibacterial; antiviral; antiallergic; cytostatic; cardiant; cerebroprotective; immunosuppressive; P2%; purinergic receptor; nervous system disorder; chronic inflammation; Alzheimer's disease, rheumatoid arthritis; amyloidosis; bacterial; viral; microbial infection; haematopoletic system disorder; immune response; autoimmune disorder; allergy; lymphoproliferative disorder; cardiac; cerebral ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P2X_7; neuroprotective; nootropic; antiinflammatory; antirheumatic;
                                                                                                                                             CCCCGTCTGGTGCCCAGTGGGAAGCTGCCTCCCATCTCAACTCCCTGAGAGCCACAGGTG
                                                                                                                                                                                                                                                                                  GATGGACTTCACAGATTTGTCCAGGCTGCCCCTGGCCCTCCATGACACACCCCCGATTCC
                                                                                                                                                                                                                                                                 CAGGAAGCIGGTCCIGTCCAGACACGTCCIGCAGTTCCTCCTGCTCTACCAGGAGCCCTT
                                                                                                                                                                                                                                                                                                                                      GCTKGCGCTGGATGTGGATTCCACCAACAGCCGGCTGCGGCACTGTGCCTACAGGTGCTA
                                                     TGGACAAACCAGAGGAGATACRGCTGCTTAGAAAGGAGGCGACTCCTAGATCCAGGGATAG
                                                                                      TGGACAACCAGAGAGATACAGCTGCTTAGAAAGGAGGCGACTCCTAGATCCAGGGATAG
                                                                                                                         CCCYGTCTGGTGCCAGTGTGGAAGCTGCCTCCCATCTCAACTCCCTGAGRGCCACAGGTG
                                                                                                                                                                                             CCTGGAGGCGCTGTGCTGCCGGAAAAAGCCGGGGGCCTGCATCACCACCTCAGAGCTGTT
                                                                                                                                                                                                                                CCTGGAGGAGCTGTGCTGCCGGAAAAAGCCGGGGGCCTGCATCACCACCTCAGAGCTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalian purinergic receptor (P2X7) useful for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Surprenant A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat P2X_7/P2Z coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0842079.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buell GN, Kawashima E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-006153/01.
P-PSDB; AAB28243.
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tuberculosis; ss
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                                                                                            CGCCAAGTACTACAAGGAAAACAATGTTGAGAAACGGACTCTGATAAAAGTCTTCGGGAT
                                                                                                                                CCGTTTTGACATCCTGGTTTTTGGCACCGGAGGAAAATTTGACATTATCCAGCTGGTTGT
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CCAGGAAATCGGAGAACTTTACAGAGGTGGCAGTTCAGGGAGGAATCATGGGCATTGA
                  GATCTACTGGGACTGCAACCTAGACCGTTGGTTCCATCACTGCCRTCCCAAATACAGTTT
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62 TGTTCGAGTACGACACGCCGCGCATCGTGCTCATCCGCAGCCGCAAAGTGGGGCCTCATGA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 AGCTGTACCAGCGGAAAGAGCCTGTCATCAGTTCTGTGCACACCAAGGTGAAGGGGGATAG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This nucleic acid sequence encodes the human purinoreceptor (HPURR), which has been shown to be similar to P2x purinoreceptors isolated from both human and rat. The nucleic acid was discovered from a spinal cord DNA library (SCORNOI) incyte clone 555697, this was found by using a search for sequence alignments of amino acids. The consensus sequence was derived from the two overlapping and/or extended nucleic acid sequences: Incyte clones 555697 and 133269. These sequences can be used in the diagnosis, prevention, and treatment of disorders and diseases of
                                                                                                                                                                                                                                                                                                Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the immune system, nervous system, cardiovascular, and of smooth muscle. For example, Alzheimer's, Huntington's, Parkinson's, Creutzfeldt-Jakob diseases, heart disease, stroke, thrombosis and other coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTTCCAGTATGAGACGAACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human purino-receptor and related nucleic acid - potentially useful for diagnosing or treating immune, nervous system, cardiovascular and smooth muscle diseases
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Pred. No. 1.5e-54;
5; Mismatches 440; Indels 36;
                                                                                                                                                                                                                                                              Purinoreceptor; HPURR; P2x; rat; spinal cord; immune system;
                                                                                                                                                                                                                                                                                                nervous system; cardiovascular; smooth muscle; Alzheimer's;
Parkinson's; Creutzfeldt-Jakob disease; thrombosis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "HPURR protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
28..1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 51-55; 66pp; English.
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AAV27197 standard; cDNA; 1762
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illarity 54.4%;
Conservative 5
                                                                                                                                                                                              HPURR nucleic acid sequence.
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P-PSDB; AAW55035.
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                                                                AAV27197;
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55 TITICCAGTATGAGACGAACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTA 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The specification describes nucleic acids encoding a functional human purinoreceptor polypeptides PXX2 and PXX4. P2X polypeptides and polynuclectides are used to identify modulators, which may be used to treat and prevent pain, diseases of the nueroendocrine system, and auditory and vestibular disorders. P2X and P2X polynuclectides are a source of probes and primers, which may be used to identify homologous sequences, for gene localisation studies, and for gene therapy purposes. The polynuclectides may also be used to produce the polypeptide recombinantly. The P2X polypeptides are used to arise antibodies, and to identify inhibitors. The present sequence encodes human P2X4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated polynucleotides, used to produce PX2 receptor polypeptides and identify potentially therapeutic compounds, encode a human P2X2 receptor polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 CAGAGGTGAAAGAGGAGATCGYGGAGAATGGAGTGAAGAAGTTGGTGCACAGTGTCTTTG
Human; purinoreceptor; P2X2; P2X4; pain; nueroendocrine disease; auditory disease; vestibular disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 235.4; DB 22; Length 1206;
Pred. No. 3.5e-54;
5; Mismatches 441; Indels 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Niforatos W,
                                                                                                                                                                                             /*tag= a
/product= "purinoreceptor P2X4"
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                                                                                                                                 Location/Qualifiers
21..1187
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54.3%;
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98US-0137458.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABBO ) ABBOTT LAB.
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  241
                                                  CAGAGGTGAAAGAGGAGATCGYGGAGAATGGAGTGAAGAAGTTGGTGCACAGTGTCTTTG 291
                                                                                                        CTGTGACCAACACTTCTAAACTTGGATTCCGGATCTGGGATGTGGGGGATTATGTGATAC 301
                                                                                                                                                              351
                                                                                                                                                                                                                                                                   352 TCAAAACAGAAGGCCAAGAGCAGCGGTTGTCCCCGAGTATCCCACCCGCAGGACGCTCT 411
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                                                                                                                                                           104 GIAAAICAGAIGCCAGCIGIACTGCCGGCTCIGCCGGCACCCACCAACGAGGTCICAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCATCGAGGCAGTGGAAGAGGCCCCCGGGCCTGCTCTTGAACAGTGCCGAAAACTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        592 CIGIGCICAICAAGAACAATAICGACITCCCCGGCCACAACTACACCACGAGAAACAICC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                880 TGTCCTTGTACCCTGGCTACAACTTCAGATACGCCAAGTACTACAAGGAAAACAATG---
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                                                                                                                   CGGTGGAGGATGACACACGTGCCACAACCTGCTTTTTAAAGGCTGCAGAAACTTCA 576
                                                                                                                                                     TGTACCTTCCACAGACTCAGAATCCAC 699
                                                                                                                                                                                                      637 TICCCAACAICACCACTACTIACCICAAGICGIGCAITIAIGAIGCIAAAACAGAICCCI 696
                                                                                                                                                                                                                          700 AGIGICCCATITICCGACTAGGAGACATCITCCGAGAAACAGGCGAIAAITITICAGAIG 759
                                                                                                                                                                                                                                                697 TCTGCCCCATATTCCGTCTTGGCAAAATAGTGGAGAACGCAGGACACGGTTTCCAGGACA 756
                                                                                                                                                                                                                                                                      KGCCAATICAGGCCGGAATAATGGGCATTGAGATCTACTGGGACTGCAACCTAGACCGTT 819
                                                                                                                                                                                                                                                                                                                 820 GGTTCCATCACTGCCRTCCCAAATACAGTTTCCRTCGCCTTGACGACAAGACCAACG 879
                                                                                                                                                                                                                                                                                                                                                                                                                          937 ACGAGCAGGCACGCTCATCAAGGCCTATGGCATCCGCTTCGACATCATGTGTTTGGGA 996
                            Graantcagargccagcreracreccegcrereccegcaccacaacaacaagrercaa 456
                                                                                                                                        CTGTGCTCATCAAGAACAATATCGACTTCCCCGGCCACAACTACACCACGAGAAACATCC: 651
                                                                                                                                                                                                                                                                                                                                817 CCGCCICTCCTTGCCCAGGTACTCCTTCCGCCGCCTCGATACACGGGACGTTGACC
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         GTTCCTCTGACCGAGGTTGTAAAAAGGGATGGATGGACCCGCAGAGCAAAGGAATTCAGA
                                                                                              532 CCATCGAGGCAGTGGAAGAGGCCCCCGGCCTGTGCTCTTGAACAGTGCCGAAAACTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trauma; spinal cord; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Human brain P2X-1 receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCGGTCTGGCCRCTGTGTTCATCGACTTCCTCATC 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human brain P2X-1 receptor encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P2X receptor; treatment; trauma; inflammation; mood disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
14..1180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV09307 standard; cDNA; 1759
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This cDNA encodes a human brain P2X-1 receptor polypeptide. The P2X receptor splice variants (P2X-1, P2X-2 and P2X-3 isoforms) can be recombinantly expressed by a host cell genetically engineered with a recombinantly expressed by a host cell genetically engineered with a vector containing the encoding nucleic acids. The receptors can be used to identify agents which modulate the activity of the receptors for use in clinical conditions such as brain stroke, brain or spinal cord traumas, infection and inflammation, cognitive disorders, epilepsy, affective and mood alsorders in general, including depression, various movement disorders including parkinson's disease, Huntingtons Chorea and Schizophrenia, as well as those conditions that are associated with the development of correction, production of antibodies and products can also be used for detection, production of antibodies and production of transgenic animals as models for mutation and structure/activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIGIGACCAACACTICIAAACTIGGAITICCGGAICIGGGAIGIGGCGGAITAIGIGAIAC 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 TGTTCGAGTACGACACGCCGCGCATCGTGCTCATCCGCAGCCGCAAAGTGGGGCTCATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 AGCTGTACCAGCGGAAAGAGCCTGTCATCAGTTCTGTGCACCACCAAGGTGAAGGGGATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 AGGGCTACCAGGAAACTGACTCCGTGGTCAGCTCCGTTACGACCAAGGTCAAGGGCGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                         DNA encoding human brain P2x receptors - used to develop products for treating, e.g. brain or spinal cord traumas, infection, inflammation and mood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 18; Length 1759;
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                                                                                                WJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1759 BP; 402 A; 496 C; 480 G; 381 T; 0 other;
                                                                                                   Tomlinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches 441;
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                                                                                                MCHALE MT,
HUMAN GENOME SCI INC.
SMITHKLINE BEECHAM PLC.
                                                                                                Carpenter DJ, Livingstone CD,
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Fig 1; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.7%;
54.3%;
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                                                                                                                                                                                                WPI; 1997-549726/50.
P-PSDB; AAW47066.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGICACCGIGAACCAGACACAGAGCACCIGICCAGAGAITCCIGAIAAGACCAGCAITI 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCATCGAGGCAGTGGAAGAGGCCCCCCGGGCTGCTCTTGAACAGTGCCGAAAACTTCA 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCCAGGTTTAA-----ACATCACTTGTACCTTCCACAAGACTCA---GAATCCAC 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 717 TCCCCAACATCACCACGTCCTACCTCAAATCGTGCATTTACAATGCTCAAACGGATCCT 776
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                                                                                                                                                                                                  Rat P2x clone 3 (AAV33853) codes for the superior cervical ganglion P2x receptor (AAW04216), a ligand-gated ion channel that opens upon binding of extracellular APP. It was isolated by screening a rat testis cDNA bank with a probe obtd. by PCR amplification of testis GDNA using primers (see also AAT33857-58) based on the rat vas deferents P2x receptor DNA (AAT33857). A rat dorsal ganglion P2x receptor CDNA (AAT33854) was similarly isolated, and a human homologue (AAT33855) was also identified. The CDNA can be used to produce recombinant P2x receptors in host (e.g. COS) cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 TTTTCCAGTATGAGACGAACAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 AGCIGTACCAGCGGAAAGAGCCIGTCATCAGTTCTGTGCACACCAAGGTGAAGGGGATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGTGGAGAAACGACGTTGGCGTGCCAACGCCGGCTTTTTTAAAGGCTGCAGAAAACTTCA
                                                                                                  DNA encoding ATP P2x receptors of the purinoceptor family - for screening cpds. useful in treating epilepsy, cognition, emesis, pain, asthma, peripheral vascular disease, hypertension, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                  DB 17; Length 1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches 429; Indels
                                                                                                                                                                                                                                                                                                                                                                                Sequence 1997 BP; 470 A; 523 C; 542 G; 462 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                Score 234.6; DB ]
Pred. No. 7.5e-54;
                                                                                                                                                                         Claim 1; Fig 2; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                  12.7%;
55.5%;
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Matches 585; Conservative
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                                                   1996-030561/03.
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                                                                       P-PSDB; AAW04216
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            CCATCGAGGCAGTGGAAGGCCCCCCCGGCCTGCTCTTGAACAGTGCCGAAAACTTCA
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The present sequence is human P2X4 receptor DNA containing its open reading frame with EcoRI restriction used for subcloning. P2X receptors are ligand-gated ion channels while P2X receptors operate generally through a G-protein coupled system. P2X purinoreceptor drugs are potential therapeutic agents in several disorders including central nervous system or peripheral nervous system conditions, e.g., epilepsy, pain, depression, neurodegenerative disorders, disorders of the skeletal muscle such as neuromuscular diseases, disorders of the reproductive system, asthma, peripheral vascular disease, hypertension, immune system disorders, irritable bowel disorder, permature ejaculation, cystic fibrosis and chronic bronchits. P2Y purinoreceptors mediate the activity of extracellular nucleoide triphosphates to regulate chloride secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGTTCCTCTGACCGAGGTTGTAAAAGGGATGGATGGACCCGCAGAGGAATTC 468
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   polypeptide useful for identifying potentially therapeutic compounds that modulate or otherwise interact with P2X containing receptors
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ches 432;
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Pred. No. 9.7
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54.9%;
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TCTGCCCCATATTCCGTCTTGGCACAATCGTGGGGGACGCGGGACATAGCTTCCAGGAGA
                                            KGGCAATTCAGGGCGGAATAATGGGCATTGAGATCTACTGGGACTGCAACCTAGACCGTT
                                                                 GGTTCCATCACTGCCRTCCCAAATACAGTTTCCRTCGCCTTGACGACAAGACCACCAAGG
                                                                                                                                      CCGCCTCCCTTTGCCTGCCCAGATATTCCTTCCGGGGCCTGGACACCGGGGACCTGGAAC
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                       GTTGGTTCCATCACTGCCRTCCCAAATACAGTTTCCRTCGCCTTGACGACAAGACCACCA
ATGKGGCAATTCAGGGCGGAATAATGGGCATTGAGATCTACTGGGACTGCAACCTAGACC
                                                                                                                   GAGCCGCCTCCCTCTGCCCAGGTACTCCTTCCGCCGCCTCGATACACGGGACGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This cDNA encodes a human brain P2X-2 receptor polypeptide. The P2X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding human brain P2x receptors - used to develop products for treating, e.g. brain or spinal cord traumas, infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "48 base pair insertion to P2X-1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P2X receptor; treatment; trauma; spinal cord; infection; inflammation; mood disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MCHALE MT, Tomlinson WJ;
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148..196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             generates P2X-2 receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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SMITHKLINE BEECHAM PLC.
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                       recombinantly expressed by a host cell genetically engineered with a vector containing the encoding nucleic acids. The receptors can be used to screen for their antagonists. The products can be used to identify agents which modulate the activity of the receptors for use in clinical conditions such as brain stroke, brain or spinal cord traumas, infection and inflammation, cognitive disorders, epilepsy, affective and mood disorders in general, including depression, various movement disorders including Parkinson's disease, Huntingtons Chorea and schizophrenia, as well as those conditions that are associated with the development of chronic or acute forms of pain, or cardiac anoxia. The products can also be used for detection, production of antibodies and production of transgenic animals as models for mutation and structure/activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 AGCGGTTGTGTCCCGAGTATCCCACCGGCAGGCTCTTGTTCCTCTGACCGAGGTTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           433 AAAAGGGAIGGAIGGACCCGCAGAGCAAAGGAAIICAGACCGGAAGGIGIGIAGIRYAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             493 AAGGGAACCAGAAGACCTGTGAAGTCTCTGCCTGGTGCCCCATCGAGGCAGTGGAAGAG
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receptor splice variants (P2X-1, P2X-2 and P2X-3 isoforms) can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 227.2; DB 18; Length 1807;
Pred. No. 7.7e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches 322; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     relationship evaluations as well as in drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1807 BP; 415 A; 507 C; 493 G; 392 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 12.3
Best Local Similarity 57.1
Matches 453; Conservative
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Tue Jul

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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression of Gs is indicative of GCA.

Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GAA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation;

(4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation growtheresion of gene(s) from Gs in the tissue, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) crowdlating GAA, M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for response in a subject, exposure of a subject to a pathogen or sterile cresponse in a subject, exposure of a subject to a pathogen or sterile cresponse in a subject, exposure of a subject to a pathogen or sterile cresponse in a subject, exposure of a subject to a pathogen or sterile cresponse in a subject, exposure of a subject to a pathogen or sterile cresponse in a subject, exposure of a subject to a pathogen or sterile cresponse in a subject, exposure of a subject to a pathogen or sterile cresponse in a subject, exposure of a subject to a pathogen or sterile companies.
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                                                                                                                                                                                                                                                                                                                                                                                     viral infection; parasitic infection; protocoal infection; fundal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma: thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states
                                                                                                                                                                                                                                                                                                                      Human cDNA differentially expressed in granulocytic cells #909.
                                                                                                                                                                                                                                                                                                                                                                    granulocytic cell; DNA chip; bacterial infection;
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                                                1119 GIGACATCATAGIC 1132
1078 TCGACTTCCTCATC 1091
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reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease. Crohi's disease, ulocarative colitis, periodontal disease, also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and MS is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part for the specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                             Score 203.8; DB 24; Length 2633;
Pred. No. 2.5e-45;
5; Mismatches 342; Indels 21;
                                                                                                                                                                                                                                     Sequence 2633 BP; 582 A; 804 C; 701 G; 546 T; 0 other;
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The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL7010), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening a clivity and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, presst, stomach, lung, thyroid, cesophageal, ovarian, kidney, prostate or panoreatic cancer, estimated to account as colon, presst, stomach, lung, thyroid, cesophageal, ovarian, kidney, prostate or panoreatic cancer, estimated to account as a cancer and contains.
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                          Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carcinoma, papillary carcinoma and Wilm's tumour.
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54.8%;
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                                                                                                                                                                                                                                                                                                      Human, cancer, colon, breast, ovary, oesophagus, kidney, thyroid, stomach, lung, prostate, pancreas, carcinoma, antitumour, cancerous, cytostatic, gene therapy, antineoplastic, Wilm's tumour, adenocarcinoma,
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                                                                          ABL70017 standard; DNA; 2633 BP.
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2000US-235082P.
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Soppet DR,
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993 GGCACCGGAGGAAAAITIGACAITATCCAGCTGGTTGTGTACATCGGCTCAACCCTCTCC 1052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            693 AATCCACAGIGTCCCATTTTCCGACTAGGAGACATCTTCCGAGAAACAGGCGATAATTTT 752
                                                                                                                                                                     543 GGCATATGCAAGGAAGACAGTGGCTGTACCCCTGGGAAGGCCAAGAGGAAGGCCCAAGGG
                  483 ACCAATTTCATCGTGACCCCGAAGCAGACTCAAGGCTACTGCGCAGAGGACCACAGAAGGG
                                                                                                                                                                                                                                                  465 ATTCAGACCGGAAGGTGTGTAGTRYATGAAGGGAACCAGAAGACCTGTGAAGTCTCTGCC
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                                                              1097 GGGACCAACTACCGTCACCTCTTCAAGGTGTTTGGGATTCGCTTTGACATCCTGGGAC 1156
                                                                                                                                         GGCAAGGCCGGGAAGTTFGACATCATCCTACAATGACCACCATCGGCTCTGGAATTGGC 1216
1046 A------ATCTCTCCCAGGCTTCAACTTCAGGTTTGCCAGGCACTTTGTGGAGAAC 1096
                                                                                                              993 GGCACCGGAGGAAAATTTGACATTATCCAGCTGGTTGTGTACATCGGCTCAACCCTCTCC 1052
                                      992
                                    933 AATGTTGAGAAACGGACTCTGATAAAGTCTTCGGGATCCGTTTTGACATCCTGGTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP P2x receptor; purinoceptor; ligand-gated ion channel; agonist; antagonist; epilepsy; cognition; emesis; pain; asthma; peripheral vascular disease; hypertension; irritable bowel syndrome; premature ejaculation; cystitis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A cDNA clone (AAT33855) codes for the human urinary bladder P2x receptor (AAM04218), a ligand-gated ion channel that opens upon binding of extracellular ATP. It was isolated from a bladder cDNA library using a rat smooth muscle P2x receptor probe. Rat vas deferens, superior cervical ganglion and dorsal root ganglion P2x receptor CDNAS (AAT33852-54) have also been isolated. These CDNAS can be used to produce recombinant P2x receptors in host, esp. mammalian, cells for use in screening (ant)agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 203.8; DB 17; Length 2643;
Pred. No. 2.6e-45;
5; Mismatches 342; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding ATP P2x receptors of the purinoceptor family - for screening cpds. useful in treating epilepsy, cognition, emesis, pain, asthma, peripheral vascular disease, hypertension, etc.
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                                                                                                                                                                                                             1053 TACTICGGICIGGCCRCTGIGTICAICGACTICCI 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human urinary bladder P2x receptor cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-030561/03.
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Matches
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The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein the polynucleotide, which is a secreted EST, and the encoded protein the suitable for treating, between the melical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, haematopoiesis regulating activity, tissue growth activity, haematopoiesis regulating activity, receptor/ligand activity, haemostatic and thrombolytic cativity, receptor/ligand activity, anti-inflammentory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                         New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.
                                                                                                                                                                                                                                 Merberg
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                                                                                                                                                                                                                                 MCCOY JM,
                                                                                                                                                                                                                             Lavallie ER,
Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 276; 618pp; English
                                                                                                                98WO-US06955
                                                                                                                                                    97US-0838821
                                                                                                                                                                                        (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                               J, Jacobs K,
Spaulding V,
                                                                                                                                                                                                                                                                                     WPI; 1999-070077/06.
Homo sapiens
                                                                                                                                                    10-APR-1997;
                                    WO9845436-A2
                                                                                                              10-APR-1998;
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Racie LA, S
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210 GAIGIGGCAATICAGGIIGG 229 756 GATGKGGCAATTCAGGGCGG 775 g δŏ

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10.6%; Score 196.4; DB 20; Length 294; 98.5%; Pred. No. 9.1e-44; Live 1; Mismatches 2; Indels 0;

Query Match 10.6 Best Local Similarity 98.5 Matches 197; Conservative

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99.5%; Score 1843.8; 99.1%; Pred. No. 0;
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                                                                                                                                                                                                         Sequence 19, Application US/08842079; Patent No. 6133434; GENERAL INFORMATION; APPLICANT: BUELL, GARY N. APPLICANT: SURPRENANT, ANNMARIE APPLICANT: RAMASHIMA, ERIC; TITLE OF INVENTION: FILE REFERENCE: 1430-160
                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/08/842,079
CURRENT FILING DATE: 1997-04-28
NUMBER OS SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 1836; Conservative
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0391 ACCAGAGGAGATACRGCTGCTTAGAAAGGAGCGACTCCTAGATCCAGGGATAGCCCTGT 1450	OY 1571 GCTGGTCCTGTCCAGACACGTCCTGCAGTTCCTCCTGGTCTACCAGGAGCCCTTGCTKGC 1630	OY 1691 CTGGCGCTCCGGGACATGGCTGACTTTGCCATCTGCCCGGCTGCTGCTGCCGCTG 1750	Db 1906 CTGA 1909  RESULT 3 US-08-742-621-2 : Sequence 2. Application US/08742621	Patent No. 5856129   GENERAL INFORMATION:   APPLICANT: HILLMAN, JENNIFER L.   APPLICANT: COLEMAN, ROGER   TITLE OF INVENTION: NOVEL HUMAN PURINOCEPTOR   NUMBER OF SEQUENCES: 5   CORRESPONDENCE ADDRESS: 1		) OPERATIVE SISTEM: 105  SOFTWARE: FRACEO Version 1.5  CURRENT APPLICATION DATA:  APPLICATION NUMBER: US/08/742,621  FILING DATE: Filed Herewith  PRIOR APPLICATION DATA:  APPLICATION NUMBER:  FILING DATE:  ATTORNAY AGRNET INFORMATION:	NAME: Billings, Locy J.  REGISTRATION WURBER: 36,749  REFERENCE/DOCKET NUMBER: PF-0147 US  TELEPHONE: 415-855-0555  TELEPHONE: 415-845-4166  INPORMATION PROCEDED: 2.  SEQUENCE CHARACTERISTICS:  IENGTH: 1762 base pairs  TYPE: nucleic acid  STRANDEDNESS: single  TOPOLOGY: linear
311 CCCTTTGCAGGGAACTCTTCGTGATGACAAACTTTCTCAAAAGAGGCCAAGA 370	TGAAGGAACCAGAAGACCTGTGAAGTCTCTGCCTGCCCCATCGAGGCAGTGGAAGA 55  TGAAGGAACCAGAAGACCTGTGAAGTCTCTGCCTGCCCCATCGAGGCAGTGGAAGA 55  I II III III III III III III III II	I TIGRACTICCCCGGCCACAACTACACCAGAGAACAICCTGCCAGGTTTAAACAICAC	CCAGGAAATGGGAGGACTTTACAGGGGGGGGGGGGGGGG	CCRTCGCCTTGACGACACACCACGTGTCCTTGTACCCTGGCTACACTTCAGATA [1: 11   1   1   1   1   1   1   1   1	CCGTITIGACATCCTGGTTTTTGGCACCGGAGGAAATTTGACATATCCAGCTGCTTGT	1091 CGACASTTACTCCAGTAACTGCTGTCGCTCCCATATTTATCCCTGGTGCAAGTGCTGTCA 1150   111:	1211 GCCGACATTAAAGTATGTGTCCTTTGTGGATGAATCCCACATTAGGATGGTGAACCAGCA 1270

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997 CCGGAGGAAATTTGACATTATCCAGCTGGTTGTGTACATCGGCTCAACCCTCTCCTACT 1056
                                   55 TTTTCCAGTAFGAGACGAACAAAAGTCACTCGGATCCAGAGCAFGAATTAFGGCACCAFTA 114
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TITLE OF INVENTION: Human Purinoreceptor P2X2 and P2X4 And Methods Of E
TITLE OF INVENTION: And USE Thereof
FILE REFERENCE: 6394.05. P1
CURRENT FILNE DAFE: 1998.11
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Pred. No. 1.9e-59;
                                                                             1057 TCGGTCTGCCRCTGTGTTCATCGACTTCCTCATC
                                                                                                                                                                                ; Sequence 21, Application US/09191608
; Patent No. 6242216
                                                                                                                                                                                                                           APPLICANT: Lynch, Kevin J.
APPLICANT: Burgard, Edward C.
APPLICANT: Metzger, Randy E.
APPLICANT: Niforatos, Wende
APPLICANT: Touma, Edward B.
APPLICANT: Yan Biesen, T.
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54.3%;
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Best Local Similarity 54.39
Matches 573; Conservative
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US-09-191-608-21
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LENGTH: 1206
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                                                                                                                                                   55 ITITICCAGIATGAGACGAACAAAGICACTCGGAICCAGAGCAIGAATTAIGGCACCAIIA
                                                                                                                                                                                                                                                                    AGCTGTACCAGCGGAAAGAGCCTGTCATCAGTTCTGTGCACCAAGGTGAAGGGGGATAG
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                                                                                                                        36;
                                                                                           Length 1762;
                                                                                        Score 237; DB 2; Length 170
Pred. No. 7.9e-60;
5; Mismatches 440; Indels
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                                                                                         12.8%;
54.4%;
                                                                                                                     574; Conservative
                                              CONSENSUS
                                                                                                       Local Similarity
MOLECULE TYPE: CL
IMMEDIATE SOURCE:
LIBRARY:
                                                          US-08-742-621-2
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                                                                                                                                                                                                                       AGCTGTACCAGCGGAAAGAGCCTGTCATCAGTTCTGTGCACACCAAGGTGAAGGGGATAG 231
                                                                                                                                                                                                                                                                                                                                                                      255 AGGGCTACCAGGAAACGGACTCCGTGGTCAGCTCGGTGACCAACCCAAAGCCAAAGGTGTGG 314
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                                                                                                                                                                 Gaps
                                                                                                                                                                 36;
                                                                                                                                 Length 1997;
                                                                                                                                                                 Indels
                                                                                                                             Score 234.6; DB 2;
Pred. No. 4.4e-59;
5; Mismatches 429;
                                                                                                                               12.7%;
55.5%;
       1997 base pairs
                                                                                                                             Query Match
Best Local Similarity 55.5
Matches 585; Conservative
                         TYPE: nucleic acid
STRANDEDNESS: single
                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                             US-08-750-134A-6
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CGGTGGAGGATGACACACACACACACACACCTGCTTTTTAAAGGCTGCAGAAAACTTCA
                                                                                                        652 IGCCAGGITIAAACATCACT-----IGTACCTICCACAAGACTCAGAAICCAC
                                                                                                                                                                                                            697 ICTGCCCCATATTCCGTCTTGGCAAAATAGTGGAGAACGCAGGACACGGTTTCCAGGACA
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                                     CIGIGCICALCAAGAACAATAICGACITCCCCGGCCACAACIACACCACGAGAAACAICC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VALERA, SOLEDAD
APPLICANT: BUELL, GARY
TITLE OF INVERMION: P2x RECEPTORS (PURINOCEPTOR FAMILY)
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30
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REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 1430-116
TELECOMMUNICATION INFORMATION:
TELEPRANE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/750,134A
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08750134A Patent No. 5985603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (703) 815-4006
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 6:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 22-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5985603
GENERAL INFORMATION:
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ZIP: 22201-4714
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US-08-750-134A-6
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CTGTGACCAAC----ACCTCTCAGCTTGGATTCCGGATCTGGGACGTGGCGGACTATG 368
                                  717 TCCCCAACATCACCACGTCCTACCTCAAATCGTGCATTTACAATGCTCAAACGGATCCCT
                                                                                                        352 TCAAAACAGAAGGCCAAGAGCAGCGGTTGTGTCCCGAGTATCCCACCCGCAGGACGCTCT
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Patent No. 5985603
GENERAL INFORMATION:
APPLICANT: WALERA, SOLEDAD
APPLICANT: BOLEL, GARY
TITLE OF INTENTION: P2x RECEPTORS (PURINOCEPTOR FAMILY)
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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                                                                      369 TGATTCCAG-
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                                    CCGGAGGAAAATTTGACATTATCCAGCTGGTTGTGTACATCGGCTCAACCCTCTCCTACT 1056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 TITICCAGIATGAGACGAACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTA
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                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: P2x RECEPTORS (PURINOCEPTOR FAMILY) NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/347 7/45
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5; Mismatches 429;
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NAME: CRANFORD, ARTHUR C.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 1430-116
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/750,134
FILING DATE:
                                                                                                                                                                                                                              Sequence 6, Application US/09363745
Patent No. 6194162
GENERAL INFORMATION:
APPLICANT: VALERA, SOLEDAD
APPLICANT: BUELL, GARY
TITLE OF INVENTION: P2x RECEPTOI
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TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 6:
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LENGTH: 1997 base pairs
TYPE: nucleic acid
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US-09-363-745-6
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                                                                                                                                      993 GGCACCGGAGGAAAATTTGACATTATCCAGCTGGTTGTGTACATCGGCTCAACCCTCTCC 1052
                                                                                                                                                                      1134 GGCRAGGCCGGGRAGTTTGACATCCTCCTACAATGACCACCATCGGCTCTGGAATTGGC 1193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/363,745
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                                                                                                                                                                                                                             1053 TACTICGGICIGGCCRCIGIGTICAICGACTICCI 1087
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5; Mismatches 342;
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                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/09363745
Patent No. 6194162
GENERAL INFORMATION:
APPLICANT: VALERA, SOLEDAD
APPLICANT: BUELL, GARY
ITILE OF INVENTION: PAR RECEPTORS (
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELECOMMUNICATION INFORMATION:
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TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 10:
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ATTORNEY/AGENT INFORMATION:
NAME: CRAWFORD, ARTHUR C.
REGISTRATION NUMBER: 25,3
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Matches 447; Conservative
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PRIOR APPLICATION DATA:
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         1023 A----
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      483 ACCAATITICALGEACCCCGAAGCAGCACTCAAGGCIACTGCGCAGAGCACCCCAGAAGG 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               543 GGCATATGCAAGGACAGTGGCTGTACCCCTGGGAAGGCCCAAGAGGAAGGCCCAAGGC 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACTTCACTGTGCTCATCAAGAACAATATCGACTTCCCGGGCCACAACTACACCACGAGA 644
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                                                                                                           SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 203.8; DB 2;
Pred. No. 6.5e-50;
5; Mismatches 342;
                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: CRAWFORD, ARTHUR C.
REGISTRATION NUMBER: 25,327
REFERRENCE/DOCKET NUMBER: 1430-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4006
TELEPAX: (703) 816-4100
INPORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           APPLICATION NUMBER: US/08/750,134A FILING DATE: 22-JAN-1997 CLASSIFICATION: 536
                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             : 2643 base pairs
nucleic acid
                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 54.8 Matches 447; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                             OPERATING SYSTEM:
U.S.A.
                           22201-4714
                                                                                                                                                                                                  FILING DATE: 22 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-750-134A-10
                                                                                                                                    SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    478 AIGICTICCCAGCACACGGGGACAGCICCTITGIAGITATGACCAACTICATCGFGACC
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                                                                                                                                                                                                                                                                                                                                            Length 1837;
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches 395;
                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                            Score 159.6; DB
Pred. No. 5,8e-37
                    REGISTRATION NUMBER: 25,327
REGISTRATION NUMBER: 1430-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4006
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1837 base pairs
                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
CLONE: rat P2x from vas deferens
                                                                                                                                                                                                                                                                                                                                            8.6%;
      CRAWFORD, ARTHUR C.
                                                                                                                                                                                                                                                                                                                                                                                    434; Conservative
                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                          TOPOLOGY:
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US-08-750-134A-4
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                                                                                                                  IGGIGCCCCAICGAGGCAGIGGAAGAGGCCCCCCGGCCIGCTCTTGAACAGIGCCGAA 584
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                                                                                                                                                                                                                                                                                                                 783 AACCIGGIGGAGGAGGIGAAIGCIGCCCACAIGAAGACCIGCCICIIICACAAGACCCIG 842
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                                                                GGCATATGCAAGGAAGACAGTGGCTGTACCCCTGGGAAGGCCAAGGAGGAAGGCCCAAGGC
                                     ATTCAGACCGGAAGGTGTGTAGTRYATGAAGGGAACCAGAAGACCTGTGAAGTCTCTGCC
                                                                                                                                                                                                 AACTTCACTGTGCTCATCAAGAACAATATGGACTTCCCCGGCCACAACTACACCACGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P2x RECEPTORS (PURINOCEPTOR FAMILY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COPTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1053 TACTICGGICTGGCCRCTGTGTTCATCGACTTCCT 1087
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APPLICATION NUMBER: US/08/750,134A
FILING DATE: 22-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
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Patent No. 5985603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: VALERA, SOLEDAD
APPLICANT: BUELL, GARY
TITLE OF INVENTION: P2x RECEI
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSE:
ADDRESSEE: NIXON & VANDERHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A. ZIP: 22201-4714
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.AGGAAAAGCAGAAAGCAAAGGTATTCGCACAGGCA. SGAACCAGAAGACTGTGAAGTCTCTGCCTGGTGCCCATCG. 	Db 718 AFGACAGATCCCAGCCTTCTTCTCTCGGGGCTGAGACTTCACCTTTCATCA 777  Qy 604 AGACAATATCCAGCTTCTCTTCGTGAGGACACACTCGCCTCTTCATCA 663    1	Db 958 GTGGGGTGGTTGGTACCATTGACTGGACTGGACTGGCACTTGGGACT 1017  QY 832 GCCRTCCCAAATACAGTTTCCRTGGCCTTGACGACAGACTGGCACTTGTACC 891	Db 1189 ACATCATCCTACTATGACTACTATGGGTTCGGATTGGAGTGGCCACAG 1248  QY 1072 TGTTCATCGATTCCT 1087	TITLE OF INVENTION: Wacleic Acids Encoding A Functional TITLE OF INVENTION: Wacleic Acids Encoding A Functional TITLE OF INVENTION: Human Purinoreceptor P2X3 and P2X6 And Methods Of Production TITLE OF INVENTION: Human Purinoreceptor P2X3 and P2X6 And Methods Of Production TITLE OF INVENTION: And Use Thereof FILE REPERBNCE: 6293.US.P1 CURRENT APPLICATION NUMBER: US 09/008,526 EARLIER PILING DATE: 1998-11-16 EARLIER FILING DATE: 1998-01-16 EARLIER FILING DATE: 1998-01-16 EARLIER PILING DATE: 1998-01-16 EARLIER APPLICATION NUMBER: US 60/071,669 EARLIER APPLICATION NUMBER: US 60/071,669 EARLIER RILNG DATE: 1998-01-16 SARLIER FILING DATE: 1998-01-16 SARLIER FILING DATE: 1998-01-16 SARLIER FILING DATE: 1998-01-16 SARLIER FILING DATE: 1998-01-16 SOFTWARE: FASTER FILING DATE: 1998-01-16 SOFTWARE: FASTER FILING DATE: 1998-01-16 NUMBER OF SEQ ID NOS: 32 SOFTWARE: FASTER FASTER FOR Windows Version 3.0
AN 1012 ACATTATCCAGCTGGTTGTACATCGGCTCAACCCTCTTCGGTCTGGCCRCTG 1071	RESULT 10 US-09-363-745-4 Sequence 4, Application US/09363745 Patent No. 6194162 GENERAL INFORMATION: TITLE OF INVERNATION: TITLE OF INVERNATION: DAPLICANT: BUELL, GARY TITLE OF INVERNATION: PZX RECEPTORS (PURINOCEPTOR FAMILY) NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS: ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON STRYET: VIRGINIA COUNTRY: U.S.A.	PE: 1-4714 PE: 1-10PP; Comg IBM FC Comg IBM FC Comg IS SYSTEM: PC PATCHIN R PLICATION DAIL PC: CON NUMBER: UTE: ATION: CATON NUMBER: UTE: ATION: ATIHUTE ION NUMBER: UTE: ATIMUTE ATIHUTE ION NUMBER: UTE: ATIMUTE ATIHUTE ION NUMBER: UTE: AND AND ATIHUTE ION NUMBER: UTE: AND AND ATIHUTE ION NUMBER: UTE: AND AND AND ATIHUTE ION NUMBER: UTE: AND	3ER: WMATIC 1100 55-4006 1100 55: 48: 48: 48:	Similarity 50.7%; Pred. No. 5.8e-37;  Conservative 6; Mismatches 395;  AGGAGATCGTGAGAATGGAGTGAAGAAGTTGCTGCACAGT

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GTTTTTGGCACCGGAGGAAATTTGACATTATCCAGCTGGTTGTGTACATCGGCTCAACC 1046
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APPLICANT: BUELL, GARY
TITLE OF INVENTION: EX RECEPTORS (PURINOCEPTOR FAMILY)
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                             Score 148; DB 4; Le
Pred. No. 1.2e-33;
3; Mismatches 273;
  EARLIER APPLICATION NUMBER: US 09/008,185
FEARLIER FILING DARF: 1998-01-16
EARLIER APPLICATION NUMBER: US 60/071,298
EARLIER FILING DATE: 1998-01-16
FEARLIER FILING DATE: 1998-01-16
NUMBER OF SEQ ID NOS: 32
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15
EENGTH: 1243
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                                                                                                                                                                                                                                                                             tch al Similarity 54.9%; 361; Conservative
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                                                                                                                                                                                                                   ) ORGANISM: Homo sapiens
US-09-191-136-15
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US-08-750-134A-8
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Patent No. 6214581
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Lynch, Kevin J.
APPLICANT: Burgard, Edward C.
APPLICANT: Burgard, Edward C.
APPLICANT: Van Biesen, T.

TITLE OF INVENTION: Nucleic Acids Encoding A Functional
TITLE OF INVENTION: And Use Thereof
FILE REFERENCE: 6293.US.P1
FILE REFERENCE: 6293.US.P1
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                                                                                                                                  Score 148.4; DB 4;
Pred. No. 9.4e-34;
}; Mismatches 274;
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CURRENT FILING DATE: 1998-11-13
EARLIER APPLICATION NUMBER: US 09/008,526
EARLIER FILING DATE: 1998-01-16
                                                                           OTHER INFORMATION: Sequencing Primer
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                                                                                                                                    8.0%;
                                    ORGANISM: Artificial Sequence
                                                                                                                                                                             362; Conservative
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US-09-191-136-15
LENGTH: 1272
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                    TYPE: DNA
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1016 TATCCAGCTGGTTGTGTACATCGGCTCAACCCTCTCCTACTTCGGTCTGGCCRCTGTGTT 1075
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    876 TCTGGGTATTAAGATCGGCTGGGTGTGCGATCTAGACAAGGCCTGGGACCAGTGCATCCC 935
                                             839 CAAATACAGTITCCRTCGCCITGACGACAAGACCACCAACGIGTCCTTGTACCCIGGCIA 898
                                                                                   936 TAAATATTCCTTCACTCGGCTGGATGGAGTTTCTGAGAAAAGCAGTGTTTCCCCTGGCTA 995
                                                                                                                          899 CAACTICAGATACGCCAAGTACTACAA---GGAAAACAATGTIGAGAAACGGACTCTGAT 955
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches 376;
                                                                                                                                                                                                                                                                                                                                                                                                       CTGTGACATCATCTGCTCAATTTCCTCA 1204
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/750,134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/09363745 Patent No. 6194162
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STREET: 1100 NORTH GLEBE ROAD
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: CRAWFORD, ARTHUR C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: VALERA, SOLEDAD
APPLICANT: BUELL, GARY
TITLE OF INVENTION: P2x REC
NUMBER OF SEQUENCES: 11
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ATTORNEY/AGENT INFORMATION:
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LENGTH: 1753 base pairs
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Matches 457; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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STRANDEDNESS:
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US-09-363-745-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,134A
FILING DATE: 22-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.6%; Score 140.2; DB 2; 52.6%; Pred. No. 3e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 1430-116
TELECOMMUNICATION INFORMATION.
TELEPRAN: (703) 816-4100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1753 base pairs
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                     25,327
                                                                                                                                                                                                                                                                                                          ATTORNET/AGENT INFORMATION:
NAME: CRAWFORD, ARTHUR C.
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Matches 457; Conservative
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                                                              VIRGINIA
                                                                                 COUNTRY: U.S.A. ZIP: 22201-4714
                                          ARLINGTON
                                                                                                                                                                                                                                                                    FILING DATE: 22
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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GGTTTTTGGCACCGGAGGAAATTTGACATTATCCAGCTGGTTGTGTACATCGGCTCAAC 1045
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                                                                                                                                                                                               Score 140; DB 4; Lk
Pred. No. 3e-31;
5; Mismatches 340;
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FILE REFERENCE: 6394.US.P1
CURRENT APPLICATION NUMBER: US/09/191,608
CURRENT FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14.
LENGTH: 1421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          completed: July 18, 2003, 23:00:59
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                                                                                                                                                                                                                                    Conservative
                                                                                                                                                Homo sapiens
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402; Conserva
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Job time : 104 secs
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Best Local Si
Matches 402,
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                                    314 ITTGCAGGGAACTCTTTCT---TCGTGATGACAAACTTTCTCAAAACAGAAGGCCAAGA 370
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Patent No. 624216
GENERAL INFORMATION:
APPLICANT: Lynch, Kevin J.
APPLICANT: Mergard, Edward C.
APPLICANT: Metager, Randy E.
APPLICANT: Niforatos, Wende
APPLICANT: Towns, Edward B.
APPLICANT: Towns, Edward B.
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US-09-191-608-14
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2: /cgn2_6/ptodata/2/pubpna/PCT_NRR_PUBB.seq:*
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6: /cgn2_6/ptodata/2/pubpna/US08_NBM_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 2, Appli Sequence 191, App Sequence 19, Appli Sequence 1, Appli Sequence 1, Appli Sequence 31290, A Sequence 31290, A Sequence 254, App Sequence 11220, A Sequence 103774, Sequence 103774, Sequence 103775, Sequence 1047, App Sequence 1742, App Sequence 250, App Sequence 250, App Sequence 250, App
SUMMARIES	US-09-977-221-2 US-10-175-523-191 US-09-833-082-1 US-09-969-347-225 US-09-977-221-1 US-09-977-221-1 US-09-918-995-31290 US-09-9664-864-254 US-09-9663-352-11220 US-10-027-632-103774 US-10-027-632-103774 US-09-918-995-5505 US-09-998-598-1742 US-09-998-598-1742 US-09-998-508-1742
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Score	1886.6 1886.6 1886.6 20 23.7 120 23.7 1142.6 1013.6 90 89 88 99 88 89 88 89 88 89 88 89 88 89 88 88
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Sequence 445, App Sequence 120, App Sequence 130520, Sequence 130521, Sequence 130521, Sequence 110, App Sequence 110, App Sequence 110, App Sequence 11, App Sequence 1, App Sequence 1254, App Sequence 1234, App Sequence 7328, App Sequence 7329, App Sequence 1146, App Sequence 1146, App Sequence 358, App Sequence 378, App Sequence 378, App Sequence 1146, App Sequence 1146, App Sequence 30, App Sequence 20, A		99.7%; Score 1846.6; DB 12; Length 1853; imilarity 99.9%; Pred. No. 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0; AAAACGCAGGGAGGCTGTCACCATGCCGGCCTGCTGCAGCTGCAGTGATTTTCC 60
US-09-764-868-445 US-09-955-999-12 US-10-027-632-13055 US-10-157-031-61 US-09-764-891-8999 US-09-764-891-8099 US-09-764-891-8099 US-09-764-891-8099 US-09-764-891-8099 US-09-764-891-8099 US-09-764-891-8099 US-10-156-761-416 US-10-156-761-114 US-10-156-761-114 US-10-126-761-114 US-10-126-761-1138 US-10-027-632-11339 US-10-027-632-1339 US-10-027-632-7328 US-10-123-155-33-90 US-10-175-523-30	ALIGNMENTS 221 NORRIS MPOUNDS 779 64,897 25859.0	199.7%; Score 1846.6; DB 12; Length 185 imilarity 99.9%; Pred. No. 0; Conservative 1; Mismatches 0; Indels 0; AAAACGCAGGGAGGGAGGCTGTCACCATGCCGGCCTGCTGCAGCTGATGATAAAACGCAGGGAGGAGGCTGTCACCATGCCGGCCTGCTGCAGCTGATAAAACGCAGGAGGAGGCTGTCACCATGCCGGCCTGCTGCTGCTGCTGCTGATAAAACGCAGGGAGGAGGCTGTCACCATGCCGGCCTGCTGCTGCTGCTGATAAAACGCTGCTGCTCACCATGCCGGCTGCTAAAAACGCTGCTCAAGCTGATAAAAAAAA
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Patent No. US20020151480A1

GENERAL INFORMATION:
APPLICANT CHUN, MIYOUNG

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 10218
FILE REPRENDER: MAI-227

CURRENT APPLICATION NUMBER: US/09/833,082

CURRENT APPLICATION NUMBER: 2010-04-10

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FASTESEQ for Windows Version 4.0
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GENERAL INCORDANCE CANCER CANC
                                                      997 CCGGAGGAAAHTHGACAFTATCCAGCTGGTTGTGTACATCGGCTCAACCCTCTCCTACT 1056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   465 ATTCAGACCGGAAGGTGTGTRATGAAGGGAACCAGAAGACCTGTGAAGTCTCTGCC 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACTTCACTGTGCTCATCAAGAACAATATOGACTTCCCCGGCCACAACTACACCCACAGAA 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               753 TCAGATGKGGCAATTCAGGGCGGAATAATGGGCCATTGAGATCTACTGGGACTGCAACCTA 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTGCCCCATCGAGGCAGTGGAAGAGGCCCCCCGGCCTGCTCTTTGAACAGTGCCGAA 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         693 AATCCACAGTGTCCCATTTTCCGACTAGGAGACATCTTCCGAGAAACAGGCGATAATTTT 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345 AACTITCTCAAAACAGAAGGCCAAGAGCAGCGGTTGTGTCCCCGAGTATCCCACCGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACATCCTGCCAGGTTTAAA-------CATCACTTGTACCTTCCACAAGACTCAG
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                                                                                                                                                                       1064 TAGGCATGGCGACCGTGCTGTGTGACATCATAGTC 1098
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Pred. No. 2e-53;
5; Mismatches 342;
                                                                                                                          1057 ICGGICIGGCCRCIGTGTICAICGACTICCICAIC
                                                                                                                                                                                                                                                                                               Sequence 225, Application US/09969347
Patent No. US20020115085A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.0%;
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Best Local Similarity 54.8'
Matches 447; Conservative
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US-09-969-347-225
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LENGTH: 2633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         700 AGIGICCCALTITCCGACTAGGAGACAICTTCCGAGAAACAGGCGATAATTITTCAGAIG 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGGCAATICAGGGCGGAAIAAIGGGCAIIGAGAICTACIGGGACIGCAACCIAGACCGTI 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        824 CCGCCTCCCTGTGCTTGCCTACTTCCTTCCGCCGCTTGATACACGGGACGTTGAGC 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGAGAAACGGACTCTGATAAAGTCTTCGGGATCCGTTTTGACATCCTGGTTTTTGCCA 996
                                                                                                                                                                                                                                                TITICCAGIATGAGACGAACAAGICACTCGGATCCAGAGCAIGAATIAIGGCACCATIA 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCATCGAGGCAGTGGAAGAGGCCCCCCCGGCCTGCTCTTGAACAGTGCCGAAAACTTCA 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIGIGCICAICAAGAACAAIAICGACIICCCGGCCACAAACIACACACGAGAAACAICC 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TICCCAACATCACCACTACTTACCTCAAGTCGTGCATTTATGATGCTAAAACAGATCCCT 703
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                                                                                                                                                                                                                                                                                                                                                 AGIGGITCTICCACGIGATCATCTITTCCIACG----IITGCIITGCTCIGGTGAGTGACA 171
                                                                                                                                                                                                                                                                                                                                                                                              ACCECECCETGCAACTCCTCATCCTGGCCTACGTCATCGGGTGGGTGTTTGTGTGGGAAA 181
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                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                 36;
                                                                                                                                               Length 1389;
                                                                                                                                                                                                 Indels
                                                                                                                                               Score 237; DB 11; Dred. No. 3.9e-64; 5; Mismatches 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCCAGGTTTAAACATCACT------
                                                                                                                                             tch 12.8%; al Similarity 54.4%; 574; Conservative
                                            ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-833-082-1
                    1389
                                                                                                                                               Query Match
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Matches 574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 TGAGACGAACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAGTGGTTCTT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               766 TICAGGGCGGAATAATGGGCATTGAGATCTACTGGGACTGCAACCTAGACCGTTGGTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                Length 11270;
                                                                                                                                                                                                                                                                        NAME/KEY: modified_base;
CCATION: (5554)...(5569);
OTHER INFORMATION: This range may encompass 3 or 4 gttt repeats
US-09-977-221-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.1%; Score 113.6; DB 12; Length 515; 88.8%; Pred. No. 3.3e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HYSERCY, Inc.

APPLICANT: HYSERCY, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REPERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT APPLICATION NUMBER: US/09/235,076

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR PILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FASTEED for Windows Version 3.0

LENGTH: 515
                                                                                                                                                                                                                                                                                                                                                                                                7.7%; Score 142.6; DB 12; Length 97.9%; Pred. No. 1.3e-33; Live 2; Mismatches 1; Indels
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PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: GB 0025859.0
PRIOR FILING DATE: 2000-10-21
PRIOR APPLICATION NUMBER: GB 0108654.5
PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 97.9 Matches 142; Conservative
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                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                     SEQ ID NO 3
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                                                                                             873 ACCAACGIGICCTIGIACCCIGGCTACAACTICAGATACGCCAAGIACTACAAGGAAAAC 932
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813 GACCGITGGITCCATCACTGCCRTCCCAAATACAGITTCCRTCGCCTTGACGACAAGACC 872
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Publication No. US20030008293A1
GENERAL INFORMATION:
APPLICANT: MORTEN, JOHN EDWARD NORRIS
TILLE OF INVENTION: CHEMICAL COMPOUNS
FILE REFRENCE: PLS/009991/0283779
CURRENT APPLICATION NUMBER: US/9/977,221
CURRENT FILING DATE: 2001-10-16
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CURRENT APPLICATION NUMBER: US/09/977,221
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/244,897
PRIOR FILING DATE: 2000-11-02
PRIOR PLILING DATE: 2000-10-21
PRIOR PLILING DATE: 2000-10-21
PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATCHTIN VOLUMER: 68 0108654.5
NUMBER OF SEQ ID NOS: 4
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Publication No. US20030008293A1
GENERAL INFORMATION:
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Matches 148; Conservative
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US-09-977-221-1
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Magappan
TITLE OF INVENTION: WUCLEC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 423;
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.523
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55.5%; Pred. No. 3.2e-19,
                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/864,864
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 341
SOFTWARE: CORIXE INVENTION DISCLOSURE Database
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                                            Sequence 254, Application US/09864864
Patent No. US20020102679A1
                                                                                    GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susn L.
APPLICANT: Dillon, Davin C.
APPLICANT: Secrist, Heather
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                                                                                                                                                                                                                                                                                                                   Benson, Darin R.
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Best Local Similarity 55.55
Matches 216; Conservative
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SEQ ID NO 254
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REPERBER: 20121.53
CURRENT APPLICATION NUMBER: US/09/864,864
CURRENT FILING DATE: 201-03-23
NUMBER OF SEQ ID NOS: 341
SOFTWARE: COTIXE INVENTION DISCLOSURE DATABASE
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Pred. No. 2.3e-21;
3; Mismatches 207;
CCACGTGATCGTCTTTCCTATGTTAGATTTG 299
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Patent No. US20020102679A1
                                                                                                                                          Harlocker, Susan L.
Dillon, Davin C.
Secrist, Heather
Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.58;
                                                                                                                                                                                                                                                                                                                                                                                  Benson, Darin R.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                 Algate, Paul A. Fling, Steve P.
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280; Conservative
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                                                               RESULT 8
US-09-864-864-331
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LENGTH: 1956
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APPLICANT:
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APPLICANT:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                          725 CATCITCCGAGAAACAGGCGATAATITITCAGAIGKGGCAATTCAGGGCGGAATAATGGG 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  785 CATTGAGATCTACTGGGACTGCAACCTAGACCGTTGGTTCCATCACTGCCRTCCCAAATA 844
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: Identification and Mapping of Single Nucleotide
TITLE OF INVERTION: Polymorphisms in the Human Genome
TITLE OF INVERTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/0/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PLING DATE: 2000-07-12
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-02-24
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-10-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-08-09
PRIOR PLING DATE: 1999-08-08-09
                                                                                                                                                                                                                                                                                                                                                                            3 CAAAACGIGCAITIATGAIGCGAAAACAGAICCCIICIGCCCCAIAIICCGACIGGGAAA
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; OTHER INFORMATION: Clone ID: 48-LIB3058-028-Q1-K1-D8
US-09-960-352-11220
                                                                                                                                                                                                                                             Score 90.8; DB 11;
Pred. No. 4e-18;
2; Mismatches 114;
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Pred. No. 1.4e-17;
0; Mismatches 3;
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SOFTWARE: FastSEQ for Windows Version 4.0
                  CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11220
LENGTH: 276
FILE REFERENCE: 16511.006/37-21(10298)C
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Best Local Similarity 57.7%;
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Best Local Similarity 96.8
Matches 92; Conservative
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; ORGANISM: Human
US-10-027-632-103774
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1759 GGAAAGAGTITCCRAAGAGTGAAGGGCAGTACAGTGGCTICAAGAGTCCTTACTGAAGCC 1818

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Sequence 103775, Application US/10027532
| Sequence 103775, Application US/10027532
| GEMERAL INFORMATION:
| APPLICANT: Wang, David G. |
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide |
| TITLE OF INVENTION: Polymorphisms in the Human Genome |
| TITLE OF INVENTION: Polymorphisms in the Human Genome |
| FILE REFERENCE: 108827.129 |
| CURRENT PILING DATE: 2000-04-30 |
| PRIOR APPLICATION NUMBER: US 60/218,006 |
| PRIOR PILING DATE: 2000-07-12 |
| PRIOR PILING DATE: 2000-04-20 |
| PRIOR PILING DATE: 2000-04-20 |
| PRIOR PILING DATE: 2000-03-29 |
| PRIOR PILING DATE: 1999-11-23 |
| PRIOR PILING DATE: 1999-18* US 60/146,002 |
| PRIOR PILING DATE: 1999-08-09-88 |
| PRIOR PILING DATE: 1999-08-09
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Publication No. US20030073523A1
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERBACE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 1.4e-17;
0; Mismatches 3;
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                                                                                                        NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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96.8%;
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Best Local Similarity
Matches 92; Conserv
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US-09-918-995-5505
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                                                                                        112
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                                                                                                                            82
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APPLICANT: Xu, Jangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFRENCE: 210121.561
CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOFTMARE: COTAXA INVENTION DISCLOSURE DETABASE
SEQ ID NO 1742
LENGTH: 229
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Pred. No. 4.1e-06;
1; Mismatches 48; Indels 0
      Length 458;
Score 57.2; DB 12; Length 4
Pred. No. 2.5e-07;
2; Mismatches 205; Indels
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Best Local Similarity 62.3%;
Matches 81; Conservative J
  3.18;
                                          220; Conservative
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US-09-998-598-1742
                         Similarity
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US-09-998-598-1742
  Query Match
Best Local S
Matches 220
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515 AGTOTOTGCOTGGTGCCCOATCGAGGCAGTGGAAGAGGCCCCCCCGGCCTGCTCTTGAA 574
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                                                                                                                               Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2003
SCHTWARE: PatentIn Ver. 2.0
SEQ ID NO 250
LENGTH: 941
                                                                        and Antibodies
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Pred. No. 3.1e-05;
4; Mismatches 107;
                                                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
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LOCATION: (909)
OTHER INFORMATION: n equals a,t,g, or c
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ne : 435 secs
           Sequence 250, Application US/09764847
Patent No. US20020132767A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  OTHER INFORMATION: n equals a,t,g,
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Matches 139; Conservative
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                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
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US-09-764-847-250
US-09-764-847-250
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                                                                                                                                                                                                            TYPE: DNA
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Title: Perfect score:

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BC017458 HCmo sapi
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BC002099 Mus muscu
BD6881359 AGENCOURT
BL6887408 603315130
BF770342 RCI-TT000
BF770342 RCI-TT000
BF770342 RCI-TT000
AL446359 AJ446359
AW913297 uf54604.y
AL54452 AL54452
BE58893 396201 Ma
AB672571 voc6ec5.r
BF681932 461444 MA
AM672571 voc6ec5.r
BH681932 461444 MA
AM672571 voc6ec5.r
AA672571 voc6ec5.r
AA672571 voc6ec5.r
BH8928936 CM2 NR008
BH452007 603170249
AJ45426 AJ445426
BPS8435 CM2 NR018
BM919221 AGENCOURT
AB6501 AGENCOURT
BM409621 AGENCOURT
BM50056 uv55160.x
BB690562 uv55160.x
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BC007679
BC007679
HTC. 12712732
                                                   BE382829 601297884
BF690388 602186810
BF347290 602021043
BQ554327 H4027E01-
BG769470 60274429
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3013)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (11-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                 BG769595
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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AA713768
BE626188
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Strausberg,R.
Direct Submission
Homo sapiens.
Homo sapiens
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SOURCE
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DEFINITION
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AUTHORS
TITLE
JOURNAL
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                                                                                                                       July 18, 2003, 20:13:22; Search time 2709 Seconds (without alignments) 11077.976 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                               32308132
             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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1635 674 671.8 666.8 645.4

No. Result

532 GAACAATATCGACTTCCCCGGCCACAACTACCCGCGGGAAACATCCTGCCGGGTTTAAA 591 665 CATCACTTGTACCTTCCACAAGACTCAGAATCCACAGGTGTCCCATTTTCCGACTAGGAGA 724	785 CATTGAGATCTACTGGGACTGCAACCTAGACCGTTGGTTCCATCACTGCCRTCCCAAATA 844 712 CATTGAGATCTACTGGGACTGCAACCTAGACCGTTGGTTCCATCACTGCCGTCCCAAATA 771 845 CAGTTTCCATTGACGAACTGACACAAGACGTTGGTTCCATCACTGCGCTACCAATA 771 772 CAGTTTCCATCGCTTGACGACAAGACACACCAACGTGTCCTTGTACCCTGGCTACAATT 904 772 CAGTTTCCGTCGCCTTGACGACAAGACACACGTGTCCTTGTACCCTGGCTACAACTT 904 772 CAGTTTCCGTCGCCTTGACGACAAAACACAAGACAACAACAACAAAAAACTCTT 91 905 CAGATACGCCAAGTACTACAAGGAAAAAAAAAAAAAAAA	892 CGGGATCCGFTTTGACATCCTGCTTTTTGGCACCGGGAAATTTGATTTTTTTT		1205 GCCAAAGCCGACATTAAAGTATGTGCTTTGTGGATGAATCCCACATTAGGATGGTGAA 1264   1131 GCCAAAGCCGACATTAAAGTATGTGTCTTTTGTGGATGAATCCCACATTAGGATGGAT	5 GATGGACTTCACAGATTGTCCAGGCTGCCCTGGCCCTCCATGACACCCCCGATTCC 13 1111111111111111111111111111111111	CCCYGTCTGGTGCCAGTGGAAGCTGCCTCCAACTCCTCGAGTGCTGTGTGTG	1565   CAGGAAGCTGGTCCAGACACGTCCTGCAGTTCCTCCTGCTCTACCAGGAGCCCTT   1624
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Y, C., Brc, E., Lege Coloskey, Thomas, P., Walker, Walker	image.llnl.gov because it RNA gi: 4505552 rocessing.	SE COUNT IGIN  Suery Match Sest Local S Matches 1736	OY         5 CGCAGGGAGGCTGTCACCATGCCGGCCTGCTGCTGCTGCTGTGTTTTCCAGTA 64           Db         29 CGCAGGGAGGCTGTCACCATGCCGGCCTGCTGCTGCTGTTTTTCCAGTA 88           OY         65 TGAGACGAACAAAGTCCACTCGAGCTGATTATGGCACCATTAAGTGTTTTCTTT 124           Db         89 TGAGACGAACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAGTGTTTTT 124           Db         89 TGAGACGAACAAAGTCACTGGAACCAACAACAACAACAACAACAACAACAACAACAACA	125 CCACGTGATCATTCCTACGTTGCTTTGCTTTGGGGGACACATTACGTGCTGCGGGGCACATTACGTGCTGGGGGGACAGCTGGCGGGGGGGG	209 GAAAGAGCCTGTCATCAGTTCTGCACACCAAGGTGAAGGGGATAGCAGAGGG 245 GGAGATCGYGGAAAAGGAGGTGAAGAAGGTGACACAGTGTCTTTGACACCGG	329 CACCTTCCCTTTGCAGGGAACTCTTCTCGTGATGACAAACTTTCTCAAAACAGAGG 38: 365 CCAAGAGCAGCGGTTGTGTCCCGAGTATCCCACGCAGGACGTCTTCTTCTTCTCTCACCG 42.	449 AGGITGTAAAAAGGGATGGATGGACCCGCAGAGCAAA

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Bukazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukazyota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
I (bases 1 to 946)
NIH-MCO http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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57 Homo sapiens cDNA clone IMAGE:4158189
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
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/clone_lib="NCI_CGAP_Brn67"
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                                   1672 CCGCTGGAGGATCCGGAAAGAGTTTCCGAAGAGTGAAGGGCAGTACAGTGCTTCAAGAG 1731
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1 (bases 1 to 795)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                         1805 ICCTTACTGAAGCCAGGCACCGTGGCTCACGTCTGTAATCCCACCTTTT 1853
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Plate: LLAM12018 row: k column: 22
High quality sequence stop: 772.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/note-"Organ: skin, Vetor: pOTBT; Site_1: XhoI; Site_2: BCoRI; ORNA made by Oigo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-ONA synthesis kit (Stratagene) and Superscript IR (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243
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                                                                                            Euteleostomi;
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/clone_11b="NHL MGC_49"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics. Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI761 row: d column: 02
High quality sequence stop: 801.
I. Oganism="Homo sapiens"
//db_xref="taxon:9606"
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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90.5%;
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Mammalia; Eutheria;
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TITLE
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dr. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCL_CGAP Library."
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                                                                                                                                                                                                                                     CGCAGGGAGGGAGGCTGTCACCATGCCGGCCTGCTGCAGCTGCAGTGTTTTCCAGTA
                                                                                                                                                                                                                                                                       TGAGACGAACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAGTGGTTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAAGAGCAGCGGTTGTGTCCCGAGTATCCCACCGCAGGACGCTCTGTTCCTCTGACCG
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                                                                                                                                                              Gaps
                                                                                                                                                              31; Indels 10;
                                                                                                                            DB 12; Length 946;
                                                                                                                          Score 671.8; DB 12
Pred. No. 3.1e-170;
4; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCATTGAGATCTACTGGGACTG 805
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Best Local Similarity 94.4%;
Matches 758; Conservative
                                                                       237
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BG766449 769 bp mRNA linear EST 15-WAY-2001 602739207F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4869288 5',
                                                                                                                                                                                                                                                                                                                                            CCACGIGAICAICITITCCIACGITIGCITIGCICIGGIGAGIGACAAGCIGIACCAGCG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 CCAAGAGCAGCAGCGGTTGTGCCCGAGTATCCCACCGCAGGACGCTCTGTTCCTCTGACCG 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      660 ITAAACATCACTTGTACCTTCCACAAGACTCAGAATCCACA---GTGTCCCATTTTCCGA 716
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                                                                                                                                                                                                                                                                                   CGCAGGGAGGCAGCTGTCACCATGCCGGCTGCTGCAGTGCTGTTTTCCAGTA 72
size-selected for average insert size 2.3 kb and normalized to Rorf 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library." 238 c. 247 g. 203 t.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 GGAGATCGYGGAGAATGGAGTGGAAGTTGGTGCACAGTGTCTTTGACACCGCAGACTA
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                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                             .;
8
                                                                                                                                                                  Score 645.4; DB 13; Length 932;
Pred. No. 4.2e-163;
3; Mismatches 34; Indels 8;
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                                                                                                                                                                        34.8%;
94.1%;
                                                                                                                                                                      Query Match
Best Local Similarity 94.1:
Matches 712; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BI603534 932 bp mRNA linear EST 07-SEP-2001 603244436Fl NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5286944 5',
                                                                                                                                                                                                         648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                 AATAATGGGCATTGAGATCTACTGGGACTGCAACCTAGACCGTTGGTTCCATCACTGCCR
                                                                                                                                                                  CAGTGGAAGAGGCCCCCCGGGCCTGCTCTTGAACAGTGCCGAAAACTTCACTGTGCTCA
                                                                                                                                                                                                                                          TCAAGAACAA-TATCGACTTCCCGGCCACAACTACACCACGAG-AAACATCCTGCCAGG
                                                                                                                                                                                                                                                                                                                                                                                           TAGGAGA-CATCTTCCGAGAAACA-GGCGATAATTTTTCAGATGKGGCAATTCAGGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         829 GAATATGGGCATTGAAATTACCTGGGACTGGCACCTAGAACGTGGTTCCATCAATGTACA
             ACCGAGGTTGTAAAAAGGGATGGATGCACCCGCAGAGCAAAGGAATTCAGACCGGAAGGT
                                                                                        GTGTAGTRYATGAAGGGAACCAGAAGACCTGTGAAGTCTCTGCCTGCTGCCCCCATCGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 932)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            836 TCCCAAATACAGTTTCCRTCGCCTTGACGACAAGAC 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 889 TCCAAACAGTTCCGACGCCTGACAGAAGACACCAC 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="hypothalamus"/lab_host="DH10B"
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/clone="IMAGE:5286944"
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Location/Qualifiers
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TITLE
JOURNAL
COMMENT
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BI603534
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Email: cgapbs-remail.nib.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNR.Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNR.Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNR Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAMI1769 row: p column: 01
High quality sequence stop: 711.
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/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Sall-XhoI (gtcggg pBluescript KS+); Site_1: BamHI; Site_2: Sall-XhoI (gtcggg ); Oligo-dr primed using primer 5'-TTTTTTTTTTTTTTTTTTVN-3', Size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for fill-length clones and constructed using the for fill-length clones and constructed using the
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                            GTAGTRYATGAAGGGAACCAGAAGACCTGTGAAGTCTCTGCCTGGTGCCCCCATCGAGGCA
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
     30.4%; Score 564; DB 13; Length 860;
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/tissue_type="hypothalamus"
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BI598073.1 GI:15491012
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/lab_host="DH10B (phage-resistant)"
/note="Grgan: skin; Vector: porarl; site_1: XhoI; site_2:
EcoRI: cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/AhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size selected >500bp for average insert size
I.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
II.RT (Life Technologies). Note: this is a NIH_MGC
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NATIONAL Institutes of Health, Mammalian Gene Collection (MGC)
NATIONAL Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATC/CCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://mage.libl.gov
Plate: LLCM1740 row: m column: 01
High quality sequence stop: 654.
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                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 769)
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Pred. No. 3.2e-156;
3; Mismatches 25;
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/clone="IMAGE:4869288"
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/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="melanotic melanoma,"
/lab_host="melanotic melanoma,"
/lab_host="melanotic melanoma,"
/note="doran: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by Oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCAGAGG(G). Size=selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using %AP-CDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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                                                                                                                                                                                                                                                                                                                                                                                                       841;
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 553.8; DB 12, Pred. No. 2.3e-138;
                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                07
                                                                                     /organism="Homo sapiens"
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                                                                                                                                    /clone_lib="NIH_MGC_49"
                                High quality sequence stop: 601.
                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:4877545"
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                LLCM1762 row: e
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91.4%;
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BG769595
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 841)
NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                       232 CCACGIGAICAICITITCCIACGITIGCITIGCICIGGIGAGIGACAAGCIGIACCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                      CACCTTCCCTTTGCAGGGGAACTCTTTCGTGATGACAAACTTTCTCAAAACAAGG
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                                  Indels
, 4e-141;
- 18;
              Pred. No. 4e-1.
3; Mismatches
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Context: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gow
Fissue Procurement: ArCc/AcTD/DTP
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            95.98;
                              629; Conservative
            Local Similarity
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BG769595
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/clone="IMAGE: 3628076"
/clone="IMAGE: 3628076"
/clone=lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage=resistant)"
/note="Corgan: brain; Vector: pOTB); Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis Kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      601297884F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628076 5', marka sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 817)
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High quality sequence stop: 646.
Location/Qualifiers
1. .817
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                                                                                                                                                                                                                                                                                   543 GIGGAAGAGGCCCCCCGGCCIGCICITTGAAC-AGIGCCGAAAACITCACIGIGCTCAI
GGAGATCGYGGAGAATGGAGTGAAGAAGTTGGTGCACAGTGTCTTTGACACCGCAGACTA
                                                                                       CACCTTCCCTTTGCAGGGGAACTCTTTCTTCGTGATGACAAACTTTCTCAAAACAGAAGG
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 662 AAACATCACTTGTACCTTCCACAAGACTCAGAATCCACAGTGTCCCATT 710
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/db_xref="taxon:9606"
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Tissue Procurement: ATCC
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//clone_lib="NIF_MGC_49"
//tissue_type="melanotic melanoma, high MDR (cell line)"
//lab_host="melanotic melanoma, high MDR (cell line)"
//lab_host="DH10B (phage-resistant)"
//note="Organ: Skin; Vector: poTBF; Site_l: XhoI; Site_2:
ECORI; CDRA made by oligo-dT priming. Directionally cloned
into EcoRI;XhoI sites using the following; S daghtor:
GGCAGCAG(G): Size-selected >500Dp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
Library. | "
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                                                                                                                                                                            BF689446 908 bp mRNA linear EST 22-DEC-2000 602186810F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298811 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1155 row: c column: 04
High quality sequence stop: 668.
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                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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                         714 CGACTAGGAGACATCTTCCGAGAAACAGGCGATAATTTT 752
                                                    769 CGACTAGGAGACCATCTACGAGAAACGGCGGATCATTAT 807
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/db_xref="taxon:9606"
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Best Local Similarity 92.9
Matches 659; Conservative
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                                                                                                                                                                                                                          mRNA sequence.
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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JOURNAL
COMMENT
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AUTHORS
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                                                                                                                                   RESULT 9
BF689446
                                                                                                                                                                                                                                                                                      KEYWORDS
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/note-norgan: skin, Vector: porm; site_1: XhoI; Site_2: BCORI, CDNA made by Oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-ONA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1452 TGGTGCCAGTGTGGAAGCTGCCTCCCATCTCAACTCCCTGAGRGCCACAGGTGCCTGGAG 1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1512 GCGCTGTGCCGGAAAAAGCCGGGGGCCTGCATCACCCTCAGAGCTGTTCAGGAAG 1571
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                                                                                                      E 1 (bases 1 to 1022)

S NTH-MGC http://mgc.nci.nih.gov/.

L Mational Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: Gapba-rémail.nih.gov
Tissue Procurement: ATCC/PCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Information on be clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.linl.gow: c column: 04
                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NIH_MGC_49"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1572 CIGGICCIGICCAGACACGICCIGCAGIICCICCIGCICTACCAGGAGCCCIIGCIKGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1332 TTCACAGATTTGTCCAGGCTGCCCTGGCCCTCCATGACACACCCCCCGGATTCCTGGACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      475 CIGGICCIGICCAGACACGICCAGGITCCTCCTGCTGCTACCAGGAGCCCTTGCTGCGG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1022;
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Pred. No. 4.1e-120;
5; Mismatches 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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High quality sequence stop: 688.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:4298811"
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ilarity 95.0%;
Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TICCCITIGCAGGGAACICITICTICGIGAIGACAAACITICICAAAACAAGGGCCAA 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         547 AAGAGGCCCCCCGGCCTGCTCTTGAACAGTGCCGAAAACTTCACTGTGCTCATCAAGA 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGATCATCITITCCTACGTTTGCTTTGCTCTGGTGAGTGACAAGCTGTACCAGCGGAAAG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCCTGTCATCAGTTCTGTGCACACCAAGGTGAAGGGGATAGCAGAGGTGAAAGGAGAGA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGYGGAGAATGGAGTGAAGAAGTTGGTGCACAGTGTCTT-TGACACCGCAGACTACACC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 TCGTGGAGAATGGAGTGAAGTTGGTGCACAGTGTCTTGTGACACCGCAGACTACACC 303
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                                                                                                                                                                                                                                     64
(Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." 199 c 216 g 188 t
                                                                                                                                                                                                                  CGAACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAGTGGTTCTTCCACG
                                                                                                                                                                                         10 GGAGGGAGGCTGTCACCATGCCGGCCTGCTGCTGCTGCAGTGATGTTTTCCAGTATGAGA
                                                                                                                                                  102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGAGATCTACTGGGACTGCAACCTAGACCGTTGGTTCCATCACTGCCR
                                                                                                                                                    47; Indels
                                                                                                           DB 10;
                                                                                                      Score 498.6; DB 10
Pred. No. 1.9e-123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
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                                                                                                      26.9%;
81.7%;
                                                                                                                                                677; Conservative
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BQ554327 642 bp mRNA linear EST 20-JUN-2002 H4027E01-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone H4027E01 5', mRNA sequence.
BQ554327 GI:21455215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Institute on Aging/National Institutes of Health National 13.3 Cascall Drive, Suite 3000, Baltimore, MD 21224-6820, USA Email: cdna@1gsun.grc.nia.nih.gov hist clone set has been freely distributed to the community. Pleas, visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7-4k.html for details. Beq primer: -21M13 Reverse High quality sequence stop: 642
364
                                                                                                                347 CACCTTCCC-TTGCAGGGGAACTCTTTCTTCGTGATGACAAACTTTCTCAAAACAGAAGG 405
                                                                                                                                                            CCAAGAGCAGCGGTIGTGTCCCGAGTATCCCACCCGCAGGACGCTCTGTTCCTCTGACCG 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases I to 642)
VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G., Martin, P.R., Stagg, C.A., Bassey, U., Aiba, K., Hamatani, T., Kargul, G.J., Luo, A.G. and Ko, M.S. Ss.
Assembly, verification, and initial annotation of NIA 7.4K mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; This clone is among a rearrayed set of 7,407 clones from more than 20 cDNA libraries."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                    CACCTTCCCTTTGCAGGGAACTCTTTCTTCGTGATGACAAACTTTCTCAAAACAGAAGG
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                                                                                                                                                                                                                                                      425 AGGTTGTAAAAAGGGATGGATGGACCCGCAGAGCAAAGGAATTCAGAC 472
                                                                                                                                                                                                                                                                               466 AGGTTGTAAAAAGGGÄTGGATGGACCCGCAGAGGAAAAGAATTCAGAC 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NIA Mouse 7.4K cDNA Clone Set"
/sex="mixed"
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Pred. No. 9.2e-97;
3; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="niaEST:H4027E01-5"
/db_xref="taxon:10090"
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1. .642
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/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA clone set
Unpublished (2002)
Other_ESTS: H4027E01-3
Contact: Yong Qian
Laboratory of Genetics
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80.2%;
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E. I. (bases 1 to 53)

S. NIH-MGC http://mgc.nci.nih.gov/

I. Upublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs.rdmail.nih.gov

Tissue Procurement: David N. Louis, M.D.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed Dy: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Plate: LiAM9429 row: f column: 12

High quality sequence stop: 543.

High quality sequence stop: 543.

Irree
                                                                                                                                                                                                                                                      BF347290 543 bp mRNA linear EST 22-NOV-2000 52021143F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 CGCAGGGAGGCTGTCACCATGCCGGCCTGCTGCAGCTGCAGTGATGTTTTCCAGTA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 TGAGACGAACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAGTGGTTCTT 124
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                          5 CGCAGGGAGGCTGTCACCATGCCGGCCTGCTGCAGCTGCAGTGTTTTCCAGTA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NOI_CGAP Library."
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                                                                                                                       235 TGAAGCCAGGCACCGTGGCTCACGTCTGTAATCCCAGCGCTT 194
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Pred. No. 5.1e-105;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4156427"
                                                                                                                                                                                                                                                                                                  5', mRNA sequence.
BF347290
BF347290.1 GI:11294885
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GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. i.brary constructed by Linq Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis Kit (Stratagene) and Supersoript II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF347097 1555 bp mRNA linear EST 22-NOV-2000 602020852F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156452
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                                                                                                                                                                                                                                                                                                                                                           TGAGACGAACAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAGTGGTTCTT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAAGAGCCTGTCATCATCTGTGCACACCAAGGTGAAGGGGATAGCAGAGGTGAAAGA 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 GGAGATCGYGGAGAATGGAGTG -- - AAGAAGTTGGTGCACA - GTGTCTTTGACACCGCAG 300
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MIH-MGC http://mgc.noi.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                CAGAAGGCCAAGAGCAG - CGGTTGTGTCCCGAGTATCCCCACCCG - CAGGACGC - TCTGTT
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  into EcoRI/XhoI sites using the following 5' adaptor:
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                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                  Length 783;
                                                                                                                                                                                                                                         16; Indels
                                                                                                                                                                                                  DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
                                                                                                                                                                                                  Score 390.2; DB 1 Pred. No. 3.6e-94;
                                                                                                                                      149 t
                                                                                                                                                                                                                                       3; Mismatches
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BF347097.1 GI:11294692
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94.1%;
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206 c
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Matches 479; Conservative
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: Xho1; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                                                                                                                                                                                                                                                                                                                                                                       CTCCTGCTCTACCAGGAGCCCTTGCTKGCGCTGGATGTGGATTCCACCAACAGCCGGCTG 1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG769470 783 bp mRNA linear EST 15-WAY-2001 602742429F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4872270 5',
                                                                                                                                                                                                                CAACTCCCTGAGGCCACAGGTGCCTGGAGGCGCTGTGCTGCCGGAAAAAGCCGGGGGCC 1541
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1662 CGGCACTGTGCCTACAGGTGCTACGCCACCTGGCGCTTCGGCTCCCAGGACATGGCTGAC 1721
                                                       CICCATGACACCCCCCGAITCCTGGACAACCAGAGGAGATACRGCTGCTTAGAAAGGAG 1421
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241 CGCCTACCGGAGCAACGCAGGCCCTGGAGGAGCTGTGCTGCCGGAGGAAGCCGGGGGGG 300
                                                                                                                                                                                                                                                                                                                  361 crccrccrrraccaggarccrrgcregrecressesangagecaccaccaccagere 420
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 783)
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National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNNL at:
http://image.llnl.gov
Plate: LLCM1748 row: i column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-rémail.nih.gov
Tissue Procurement: ArC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Location/Qualifiers
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://mage.llnl.gov
Plate: LiAM8429 row: g column: 13
High quality sequence start: 39
High quality sequence stop: 541.
Location/Qualifiers
1. 555
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Search completed: July 18, 2003, 22:59:07 Job time: 2716 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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July 18, 2003, 15:41:30 ; Search time 4799 Seconds (without alignments) 11237.237 Million cell updates/sec US-09-977-221-2 1853 1 aaaacgcagggaggggggct......cgtctgtaatcccaccttt 1853 Total number of hits satisfying chosen parameters: 2054640 seqs, 14551402878 residues OM nucleic - nucleic search, using sw model IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Perfect score: Sequence: Searched: Run on:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

GenEmbl:\* Database :

em\_htg\_hum:\*
em\_htg\_inv:\*
em\_htg\_other:\*
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em\_htg\_rod:\*
em\_htg\_mam:\* gb\_ba:\*
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ALIGNMENTS

linear PAT 20-JUN-2002 DNA AX427649 1853 bp Sequence 2 from Patent EP1199372. AX427649 AX427649.1 GI:21537769

RESULT 1
AX427649
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ACCESSION

human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

SOURCE ORGANISM

VERSION KEYWORDS

Morten, J.E.
Polymorphisms in the human p2x7 gene Patent: EP 1199372-A 2 24-APR-2002;

REFERENCE AUTHORS TITLE JOURNAL

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/db_xref="taxon:9606"
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RLDDKTINVSLYPGYNFRYAKYYKENNVEKRTLIKVFGIREDILVFGGGGFDIJQLV
VYJOSTLSYFGLAAVFIDFLIPYSSNCCRSHYPWCKOOPCVWERYYYKKOESIV
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Direct Submission
Submitted (21-NoV-1996) G.N. Buell, Geneva Biomedical
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Craniata; Vertebrata;
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Rassendren, F., Buell, G., Virginio, C., M
The permeabilizing ATP receptor (P2X7)
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k; Pred. No. 0;
16; Mismatches
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Location/Qualifiers
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Chordata;
               Primates;
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QY	QY	Qy Db	QY	QY Dp	O.Y.	Qy	QZ Dp	Qy Dp	QY	Oy Dp	Qy	QY Dp	Q <sub>Y</sub>	Qy Up	Qy	\dagger \dagge	QY	QY
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A 1501 GGFGCCTGGAGGMGCTGTGCCGGAAAAAGCCGGGGGCCTGCATCACCACCTCAGAGC 1560	OY 1561 IGTICAGGAAGCTGGTCCTGTCCAGACACGTCCTGCAGTTCCTCCTCTACAGGAGC 1620	09 1621 CCTTGCTKGCGCTGGATGTGGATTCCACCAACAGCCGGCTGCGGCACTGTGCCTACAGGT 1680 1621 CCTTGCTGCGCTGGATGTGGATTCCACCAACAGCCGGCTGCGGCACTGTGCCTACAGGT 1680	OY 1681 GCTACGCCACCTGGGCTTCGGCTCCCAGGACTTGCCTGCC	07 1741 GCTGCCGCTGGAGGATCCGGAAAGAGTTTCCRAAGAGTGAAGGGCAGTACAGTGGCTTCA 1800	OY 1801 AGAGTOCTFACTGAAGCCAGGCACGGTGGCTCACGTCTGTAATCCCACCTTT 1853		LOCUS ARLIBOBYS 1853 DP DNA LINEAR PAT 16-YAY-2001 DEFINITION SEQUENCE 19 from patent US 6133434. ACCESSION ARLIG693. VERSION ARLI6695.1 GI:14097015	Unk Unk Unc	E 1 (bases S Buell,G.N Purinergi L Patent: U	FEATURES LOCALIDATALITIETS SOURCE 11853 /Organism="unknown" BASE COUNT 455 a 503 c 477 g 418 t	Query Match 99.6%; Score 1845; DB 6; Length 1853; Best Local Similarity 99.18; Pred. No. 0; Matches 1826. Conservative 16. Wismatches 1. Indals 0. Cana 0.	SGAGGGAGGCTGTCACCATGCCGGCCTGCTGCAGCTGCAGTGTTTTCC 60	61 AGTAIGAGACGAACAAAGTCACTCGGATCCAGGCGCGCGCGGGGGGGG	121 TCTTCCACGTGATCATCTTTTCCTACGTTTGCTTTGCTT	AGCGGAAAGAGCTGTCATCAGTTCTGTGCACACCAAGGGAAAGGGAAAGAGGGAAGCGAACCAAGCGAAAGAGAAAGAGGGATAGCAGAGGGAAACGAAAGAAA	241 AAGAGAGATCGYGGAAATGGAGTGAAGAAGTTGGTGCACGAGGTTTTGACACGCGAG	241 AMONGONOMICCIOGEGEANTICGACIGEACTICGIGEACAGIGICTITGACACCOCAGO 3 301 ACTACACCTTCCACGGGGAACTCTTTCTTCGTGATGACAAAACTTTCTCAAAAAG 3 	Db 301 ACTACACCTTCCCTTTGCAGGGAACTCTTTCTTCGTGATGACAAACTTTCTCAAAACAG 360

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/clone="MGC:2008] IAAGE:429811"
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         /organism="Homo sapiens"
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Shevchenko,Y., WetherDy,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Mastiello,C., Mastrian,S.D., Mccloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tlongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
1620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens, Similar to purinergic receptor P2X, ligand-gated ion channel, 7, clone MGC:20089 IMAGE:4298811, mRNA, complete cds. BC011913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be founthrough the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 28 Row: k Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4505552. Location/Qualifiers
1. .2164
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2164)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (30-UL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                             GGTGCCTGGAGGMGCTGTGCTGCCGGAAAAAGCCGGGGGCCTGCATCACCACCTCAGAGC
                                                                                                     GGTGCCTGGAGGAGCTGTGCTGCCGGAAAAAGCCGGGGGCCTGCATCACCACCACGAGGC
                                                                                                                                                               TGTTCAGGAAGCTGGTCCTGTCCAGACACGTCCTGCAGTTCCTCCTGCTCTACCAGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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MGC

VERSION KEYWORDS

ORGANISM

REFERENCE

AUTHORS JOURNAL

REMARK COMMENT

DEFINITION

RESULT 4 BC011913

ACCESSION

source

FEATURES

0.0   0.0	QY         1556 AGAGCTGTTCAGGAAGCTGGTCCTGTCCAGACTGCTCTCCTGCTGCTCTACCA 1615           Db         1474 AGAGCTGTTCAGGAAGCTGGTCCTGCAGACACGTCCTGCAGTTCCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	OY 1676 CAGGTGCTACGCCACCTGGGCTTCGGCTCCCAGGACATGGCTGACTTTGCCATCCTGC 1735	3100 3100 5 fr		SOURCE 1.3340  BASE COUNT 919 a 958 c 899 g 764 t  ORIGIN  Query Match 69.2%; Score 1282.4; DB 6; Length 3540;  Best Local Similarity 81.4%; Pred. No. 0;  Matches 1469; Conservative 12; Mismatches 323; Indels 0; Gaps 0;	11 GAGGGAGGCTGTCCCGGCCTGCTGCAGCTGCAGTGATGTTTCCAGTATGAGAC 70	156   AAACAAAGTCACCGGATCCAGAGCGTGAATTACGGCACCATCAAGTGGATCTTGCACAT   225     131   GATCATCTTTCCTACGTTTGCTTTGCTGGTGAAGTGACTGTACCAGCGGAAAGA   190     1
	334 CCAGAAGACCTGTGAAGTCTCTGCCTGGTGCCCCATCGAGGCGCAGTGGAAGAGGCCCCCCG 393  560 GCCTGCTCTCTTGAACAGTGCCGAAAACTTCACTGTGCTCATCAAGAACAATATCGACTT 619  1111111111111111111111111111111111	CCACAAGACTCAGAATCCACAGTGTCCTGCACTAGGAGACATCTTGTACCTTTCCGACAACACCAGAAACTTTCCGACTAGGAGACATCTTCCGAGAAACTTTCCGACTAGGAGACATCTTCCGAGAACATCTTCCGACAACAACAACAAACA	GACCGTTGGTTCATCATGCCETCCCAATAC GACCGTTGGTTCCATCACTGCCGTCCCAAATAC ACCAACGTGGTCCTTGTACCTGGCTACAACTTC ACCAACGTGTCCTTGTACCTGGCTACAACTTCAACTTCAACTTCAACGTACAACTTCAAAACTTCAAAAAAAA		1065GCORCIGIGIT 1075 934 GITIGGAGAAGGAAGTGACTAACGCAGCGTTGTCTCCCCCAGGCCACTGTGTT 993 1076 CATCGACTTCCTCATCGACASTTACTCCAGTAACTGCTGTCTCCCCATATTTATCCCTG 1135	GTGCAAGTGCTGTCAGCCTGTGTGGTCAACGAATACTACTACAGGAAGAAGTGCGAGTC	STGTCCTTTGT CTGCAAGATGT CTGCAAGATGT CTGCAAGATGT AGGCTGCCCCT AGGCTGCCCCT AGGCTGCCCCCT

	15		Actual.  (Dases 1 to 3540)  Surprenant, A., Rassendren, F., Kawashima, E., North, R.A. and Buell, G. The cytolytic P22 receptor for extracellular ATP identified as a P2x receptor (P2X7)  Science 272 (5262), 735-738 (1996)  96202420  9614837  (Dases 1 to 3540)  Direct Submission  Direct Submission  Submitted (26 FERR-1996) G. N. Buell, Glaxo. Molecular Biology. 14	chemin des Aulx, 1228 Plan-les-Ouates, Geneva, SWITZERLAND Location/Qualifiers 1. 3540 /organiam="Rattus norvegicus" /isolate="Ma3" / db xref="taxon:10116" /dev_stage="adult" 1221909 /gene="P2X7" 1221909 /gene="P2X7" /function="APP ligand gated ion channel" /codon_start=1 /protein_id="CaA65131:1"
4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	6 6 6 6 6 6 6 6 6	RESULT 8 IMP2X7GEN IMP2X7GEN IMP2X7GEN ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL	FEATURES SOUTCE GENERAL CDS
QY         251 CGTGGAGATGGAGTGGTGCCACAGTGTTTGACCCGCAGACTACACTT 310           DD         346 CACGGAGGGGGGGGGGAGTGAGTGTGTTTGACCCGCACTACACTT 41           DD         346 CACGGAGGGGGGGGGGAGTGAGACTTTCTCACACACTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTAC	09         491 TGAAGGGAACCAGAAGACCTGTGAAGTCTGCTGGTGCCCCATCGAGGCAGA 550           11	QY         791 GATCTACTGGGACTGGACCTGGCTTGGTTCCATCACTGCCRTCCCAAATACAGTT         850           Db         886 GATCTACTGGGACTGCACCTGGACAGCTGGTCCATCCCAAATACAGCT         945           QY         851 CCRTCGCTTGCAACACAGCTGGTCCTTGTACCTGGCTACAACTTCAGATA         910           Db         946 CCGCCGGCTGGACAACACACAATACACTCCTGGCTACAACTTCAGATA         100           QY         911 CGCCAGGTGAACAAAAACAATGTTGAAAAACGGCTGTGATAAAACTCTTGGGGAT         1005           QY         911 CGCCAAGTACTACAAGGAAAAACAATGTTGAGAAACGGACTTCGGGAT         1005           Db         1006 CGCCAAGTACTATAAAGGAAAACGAAAAACGAAAAACGAATGAAAAACGAATACAAAACCTTCGGCGT         1065	971 CCSTTTTGACATCTGGTATTTTGGCACCGAGGAAANTTGACATTATCCAGCTGTTTT 1030 1111111111111111111111111111111111	GCCCTGTGGGCGAACGAATACTACTACGGAAGGAGGGGGGCCATTGTGGAGCCAAA 121

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RIDDKYTUNESLFPGYNETRAKYYENOKBERRILARGGYRTDIJGIV
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                                                                                                                                                                                                    Score 1282.4;
Pred. No. 0;
2; Mismatches
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MMU9823 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM AUTHORS TITLE JOURNAL REFERENCE AUTHORS AUTHORS	TITLE JOURNAL FEATURES SOURCE Gene CDS	BASE COUNT           OREGIN           Query Match           Best Local           Matches 145           QY         27           Db         72           QY         72           QY         132           Db         132           QY         207           QY         207           QY         267           QY         267           QY         267           QY         267

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* consists of 21 contigs. The true order of the pieces r is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the flitshed sequence as soon as it is available and the accession number will be preserved.
90244 104982: coulty of 100 bp 106983 105082: gap of 100 bp 120698 120097: contig of 15615 bp in length 120688 120797: gap of 100 bp 120798 143533: contig of 22736 bp in length 120798 143533: contig of 22736 bp in length
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of 2276 bp in length
100 bp
of 2642 bp in length
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68011: contig of 11810 bp in length
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104982: contig of 14739 bp in length
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68112 77944: contig of 9833 bp in length
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21923: contig of 4399 bp in length
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1. .1071
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13173: contig of
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/clone="RP11-6F18"
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25018 25117; 9
25118 29237
29238 29337; 9
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13274 1742;
17425 17524;
17525 2192
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90244 10498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC011216 171065 bp DNA linear HTG 26-MAY-2000 Homo sapiens clone RP11-6F18, WORKING DRAFT SEQUENCE, 21 unordered pleces.
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                                                                                                                                                       AAAAAGCCGGGGGCCTGCATCACCACCTCAGAGCTGTTCAGGAAGCTGGTCCTGTCCAGA 1586
                                                                                                                                                                                                                                                                                                1587 CACGICCIGCAGIICCICCICCICCIACCAGGAGCCCIIGCIKGCGCIGGAIGIGGAIICC 1646
                                                                                                                                                                                                                                                                                                                        1332 AGGCTGTCCCTATCTCTCCACGACTCACCCCTGACTCCTGGACAATCTGAGGAAATTCAG 1391
                                              1407 CTGCTTAGAAAGGAGGGGACTCCTAGATCCAGGGATAGCCCYGTCTGGTGCCAGTGTGGA 1466
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Submitted (03-001-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, UGA
On May 25, 2000 this sequence version replaced 91:7272137.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                          1692 CAGGACATGGCCCACTTTGCCCCAGCTGCCCCTGGAGGAGGATGCCGGAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                  1647 ACCAACAGCCGCTGCGGCACTGTGCCTACAGGTGCTACGCCACCTGGCGCTTCGGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGACATGGCTGACTTTGCCATCCTGCCCAGCTGCTGCCGCTGGAGGGATCCGGAAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITCCRAAGAGTGAAGGGCAGTACAGTGGCTTCAAGAGTCCTTACTGAAGCCAG 1820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birren, B., Linton, L., Nushaum, C. and Lander, E. Homo sapiens, clone RP11-6F18
Unpublished
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Web site: http://www-seq.wi.mit.edu
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AC011216.4 GI:8072519
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96053 ACCAGGAGCCCTTGCTGGCGCTGGATGTGGATTCCACCAACAGCCGGCTGCGGCACTGTG 96112
                                               1312 TCCSAAGACCTGYGAGACTTCACAGATTGTCCAGGCTGCCCCTGGCCTCCATGACA 1371
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                              1672 CCTACAGGTGCTACGCCACCTGGCGCTTCGGCTCCCAGGACATGGCTGACTTTGCCATCC 1731
                                                                                            1732 TGCCCAGCTGCTGCCGCTGGAGGATCCGGAAGAGTTTCCRAAGAGTGAAGGGCAGTACA 1791
                                                                                                                                                       1792 GIGGCTICAAGAGICCTIACIGAAGCCAGGCACCGIGGCICACCGICIGIAAICCCACCIT 1851
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 6839)
Buell, G. N., Talabot, F., Gos, A., Lorenz, J., Lai, E., Morris, M.A. and Antonarakis, S. E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (22-APR-1997) G.N. Buell, Geneva Biomedical Research
Institute, Molecular Biology, 14 Chemin des Aulx, 1228
Plan-les-Ouates, Geneva, SWITZERLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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/clone_lib="Dupont Merck P1 library #1"
/dev_stage="adult"
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Pred. No. 6.7e-124;
7; Mismatches 7;
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/usedin=Y12851:P2X7mRNA
1462 c 1523 g 1798
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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5465, .5962
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     Homo sapiens P2X7 gene,
Y12855
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1516. .1617
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ilarity 97.4%;
Conservative 7
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                                                                                                                                                                                                                                                                                                                                                                            Y12855.1 GI:2612785
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Homo sapiens.
Homo sapiens
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Matches 528;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTCAGAGCTGTTCAGGAAGCTGGTCCTGTCCAGACACGTCCTGCAGTTCCTCGTGCTCT 1611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1312 TCCSAAGACCTGYGATGGACTTCACAGATTTGTCCAGGCTGCCCCTGGCCCTCCATGACA 1371
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Pred. No. 3.3e-124;
7; Mismatches 6;
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143634. 171065
/note="assembly_fragment"
40599 c 40829 g 43373 t
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9338, .34192
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56202. .68011
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6154. .8795
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8896. .13173
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13274. .17424
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fnote="assembly_fragment"
25118. .29237
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105083. .120697
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                /note="assembly_fragment"
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vector_side:right"
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Dozado, R.J., Lucier, R., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Maner, G., Miner, Z., Mitchall, T., Wohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwonou, G.,
Oragunye, N., Oviedo, R., Pirmus, E., Patton, B., Peery, J., Perez, L.,
Rives, M., Nolas, R., Rojubokan, T., Rolfe, M., Ruiz, S., Savery, G.,
Schers, E., Sonaike, T., Sparks, A., Stanerisa, R., Tamerisa, R.,
Sutton, M., Svatek, A., Tabor, P., Tamerisa, R., Tamerisa, R., Tansey, J., Taylor, C., Taylor, T., Talfrod, B., Thomas, N., Thomas, S.,
Wand, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, C., Walren, R., Washington, C., Watlington, S.,
Williams, C., Walliamson, A., Wlerson, B., Worley, K.,
Weinstock, G. and Gibbs, R., Rorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 7 contigs. The true order of the pleces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (31-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jul 25, 2002 this sequence version replaced g1:21908286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (22-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (Dases 1 to 22893)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: M13;
Chemistry: Dye-primer Bodipy: 18% of reads
Chemistry: Dye-primer Bodipy: 18% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 227917 bases at least Q40
Consensus quality: 228951 bases at least Q30
Consensus quality: 229319 bases at least Q30
Batimated insert size: 217327; sum-of-contigs estimation
Quality coverage: 11x in Q20 bases; sum-of-contigs estimation
            Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.
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2: gap of unknown length
2: contig of 2390 bp in length
3: gap of unknown length
4: contig of 6718 bp in length
5: gap of unknown length
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of 9393 bp in length
unknown length
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Drafting Center Code: BCM
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----- Summary Statistics
Sequencing vector: Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: hgsc-help@bcm.tmc.edu
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Direct Submission
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Direct Submission
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I (Dases i to 220835)

Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbraia, J., Benton, J., Binage, R., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Binage, R., Blankenburg, K., Bonnin, D., Buhay, C., Burch, F., Burkett, C., Burch, F., Burkett, C., Burch, R., Bryant, M.P., Carron, T.B., Carter, M., Cavacos, S.R., Chake, C., Chen, R., Carter, M., Cavacos, S.R., Chake, C., Chen, G., Chen, R., Chen, E., Chordan, J., Dathorne, S.R., David, R., David, R., Davida, M.L., Davis, K. R., Delqado, C., Den, A.L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, C., Escar, C., Escar, C., Escar, C., Escar, C., Corlell, G., Escar, C., Escar, C., Edgis, A., Garcia, A., Garcia, A., Garca, F., Havlak, P., Havlak, P., Havlak, P., Harnandez, C., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, C., Harris, K., Harris, C., Harris, K., Harris, C., Harris, K., Johner, Y., Johney, C., Hollins, B., Harris, C., Harris, K., Harris, C., Harris, K., Harris, C., Harris, K., Harris, C., Harris, C., Harris, C., Harris, C., Harris, K., Harris, C., Leader, M., Harris, C., Harris, C., Leader, M., Harris, C., Leader, M., Leader, M., 
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5460 IICAGAGACCIGCGAFGGACITCACAGATIFGICCAGGCIGCCCCTGGCCCTCCATGACA 5519
                                                                            1372 CACCCCCGATTCCTGGACAACCAGAGAGATACRGCTGCTTAGAAAGGAGGCGACTCCTA 1431
                                                                                                                                                                                                                                1432 GATCCAGGGATAGCCCYGTCTGGTGCCAGTGTGGAAGCTGCCTCCCATCTCAACTCCCTG 1491
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Homo sapiens chromosome 12 clone RP11-340F14, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
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/db_xref="G1:5880353"
/db_xref="G1:5880353"
/translation="MPGACGWNDVFQYETNKIIWIOSKTYGTIKWLFHVVLFSYIGFA
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FWWTNFLKTEGQEGGLCPEYPTPFILCSSDRGCKKGWLGPRSKGIQTGRCIHYNEKQK
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*** SEQUENCING IN PROGRESS ***,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGCCGGCTTGCTGCAGCTGGAATGATGTTTCCAGTATGAGACAAAAAAATCATCTGG
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                                                                                                                                                                                                                                                                                                                                                       Gaps
    Direct Submission
Submitted (07-AUG-1998) Veterinary Pathobiology, University
Missouri, 201 Connaway Hall, Columbia, MO 65211, USA
Location/Qualifiers
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                                                             1. .504 "organism="bos taurus" | /db_xref="taxon:9913" | /cell_line="bovine aortic endothelial | . .>504
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Pred. No. 1e-88;
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Rattus norvegicus clone CH230-83K8,
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/product="P2X7"
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85.78;
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AC130133/c
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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29597: contig of 8565 bp in length
29697: gap of unknown length
115777: contig of 86080 bp in length
115877: gap of unknown length
228935: contig of 113058 bp in length.
                                                                                                                                                                         607 others
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Pred. No. 8.7e-124;
7; Mismatches 7;
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Bos taurus P2X7 mRNA, partial cds.
AF083073
AF083073.1 GI:5880352
                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                Location/Qualifiers
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REFERENCE AUTHORS

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is record will be updated with the finished sequence soon as it is available and the accession number will
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  MARIND M., Addms.C., Adio-Oduola, B., Ali-Osman, F.R., Allano, C., Adishroy, D.M., Addms.C., Adio-Oduola, B., Ali-Osman, F.R., Allano, C., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allano, C., Alabbooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Bimage, K., Blankenburg, K., Bonnin, D., Bonde, J., Burket, C., Burrell, K.L., Bronn, M., Eryant, M.P., Buhay, C., Burch, P., Burket, C., Burrell, K.L., David, N.C., Coyle, M.D., Dathorne, S.R., David, R., Delado, C., Chen, Z., Chowdhy, J., Christopoulos, C., Chen, S., Chen, R., Deladod, O., Denn, A.L., Ding, Y. Dinh, H. H. Douthwaite, K.J., Daraper, H., Dayer-Carroll, L., Dederich, D. A., Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Balls, T., Eargar, D., Garcia, A., Garner, T., Garza, M., Gill, R., Gorrell, J.H., Guevra, W., Gunarahe, S., Hamilton, K., Harris, C., Harris, K., Harris, M., Havlak, P., Hawes, A., Hennodez, J., Hennadez, J., Homandez, J., Homatdez, O., Edgeon, A., Garner, T., Garza, M., Gulland, S., Gorrell, J.H., Guevra, W., House, M., Halls, B., Lewis, L.C., Lewis, L., Lozado, H., Ju, X., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Marin, E., Land, S., Martin, R., Marin, R., Mar, J., Lu, X., Lud, Y., Lud, R., Lud, R., Lud, R., Mayer, M., Mohaney, E., McLeol, M. P., Meador, M., Mayer, M., Mayhiney, E., McLeol, M. P., Meador, M., Mayhiney, E., McLeol, M. P., Meador, M., Mayhiney, E., McLeol, M. P., Meador, M., Mayhiney, B., McLeol, F., Panerisa, R., Panerisa, R., Mahhiney, E., McLeol, M., P., Meador, M., Mayer, M., Mayhiney, M., Mitcherson, E., Wakhiney, S., Oquib, M., Okwuon, G., Sodergren, E., Soche, Shen, H., Peliros, P., Peters, M., Peters, M., Paters, M., Paters,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (08-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 5676 bases at least 040 Consensus quality: 5422 bases at least 030 Consensus quality: 61794 bases at least 030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name: CH230-83K8
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Worley, K.C.
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Dicknep, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Campoplano, A., Chang, J., Campoplano, A., Chang, J., Campoplano, A., Cohangelo, M., Collins, S., Collymore, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fizzhugh, W., Gaqe, D., Galagan, J., Gardyna, Gord, S., Gordte, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Ilaev, I., Johnson, R., Jones, C., Kamat, A., Kartas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehocky, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Maneus, L., Mihova, T., Munchy, T., Waylor, J., Nguyen, C., Nicol, R., Nobu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, R., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Kiley, R., Schauer, S., Schupback, Raman, J., Rosettl, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Stause, Phomann, N., Stolanovic, N., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Pohnett for Genome
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Mus musculus clone RP23-37P22, LOW-PASS SEQUENCE SAMPLING.
ACL17579
   1672 CCTACAGGTGCTACGCCACCTGGCGCTTCGGCTCCCAGGACATGGCTGACTTTGCCATCC 1731
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Chararco, B., Choepel, Y., Canarda, J., Campoplano, A., Chang, J., Choepel, Y., Colangelo, M., Collins, S., Colymore, A., Cook, R., Cook, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Perreira, P., FitzGerald, M., FitzBugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Gordte, M., Gardyna, S., Ginde, S., Gords, S., Gardyna, S., Ginde, S., Gardyna, S., 
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 66872)
                                                                                                                                                                                          1732 TGCCCAGCTGCTGCCGCTGCAGGATCCGGAAAGAGTTTCCRAAGAGTGAAGGCCAGTACA
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Mus musculus
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74698: gap of unknown le
78658: gap of unknown le
78658: gap of unknown le
80813: contig of 2255 bp
80813: contig of 2255 bp
80813: gap of unknown le
83924: gap of unknown le
81079: contig of 2155 bp
81179: gap of unknown le
81179: gap of unknown le
81179: gap of unknown le
81139: gap of unknown le
91366: contig of 2260 bp
91366: contig of 2827 bp
91466: gap of unknown le
91311: contig of 2810 bp
97041: gap of unknown le
97041: contig of 210 bp
97041: gap of unknown le
103322: contig of 2310 bp
103322: gap of unknown le
103322: gap of unknown le
contig of 2881 b
gap of unknown i
contig of 1782 b
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115282: contig of 4426
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62659:
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TITLE JOURNAL COMMENT

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Length 66872;
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Pred. No. 3.8e-77;
3; Mismatches 102;
                                                                                                                                                                                                                                                                                                    19 19688: gap of 100 bp 100 bp
                                                        7309: gap of 100 bp 18011: contig of 702 bp in 1111: gap of 100 bp 1809: contig of 698 bp in 19588: contig of 679 bp in 19588: co
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25876: contig of 679 bp
25976: gap of 100 bp
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43258: contig of
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                                                                          Wyman, D., Ye, W.J.,
                                                                                                                                                                 Direct Submission
Submitted (18-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, UGA
ON May 18, 2002 this sequence version replaced g1:20128322.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                           Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J. Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
        Talamas, J.,
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the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
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Search completed: July 18, 2003, 18:14:43 Job time : 4814 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
                                                                                                                                    OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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			Description	CACAL Manual	ייחוומו בישע אבווב רח	Human P2X_7/P22 co	Human cDNA clone C	Human secreted pro	Rat P2X 7/P2Z codi	HPURR nucleic acid	Nucleotide sequenc	Human brain P2x-1	Rat superior cervi
SUMMARIES			ID	AAT.43007	7000 PTT 177	AAC63694	AAF98411	AAV30932	AAC63693	AAV27197	AAH25211	AAV09307	AAT33853
			8	24	1	22	22	19	22	13	22	18	17
			Match Length DB	1853	1	1853	2168	2169	3540	1762	1206	1759	1997
	ф	Query	Match	40 7		9.66	99.1	98.9	69.2	12.8	12.7	12.7	12.7
			Score	1846 6		1845	1836.2	1833.4	1282.4	237	235.4	235.4	234.6
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Human purinergic r Human brain P2X-2 Human CDNA differe Pancreas cancer re Funcreas cancer re	EST clone C0390.  DNA encoding novel Rat vas deferens P Human P2X3 puriner Human P2X3 recept Human P2X3 recept	en 😅	Human purino recep Nucleotide sequenc Human purino recep Nucleotide sequenc Human purinergic r Human purino recep Nucleotide sequenc DNA encoding novel	Nucleotide sequenc Nucleotide sequenc Human polynucleoti Coding sequence fo Coding sequence fo Human purinergic r Human ovarian tumo Human covarian tumo Human covarian tumo Human covarian tumo Ruman covarian tumo Ruman coding
AAD04979 AAV09308 ABK84338 ABL70017	AAV89619 AAS76004 AAT33852 AAX87357 AAC64099 AAD04964	AAX87356 AAC64101 AAD04966 AAL43026 AAD04988 AAL43028	AA138894 AA155132 AAH52208 AA251321 AAD04982 AAE5133 AAH5209 ABK43717	AA251324 AAH25210 AAH92047 AAV61833 AAD04978 ABK09794 ABK09794 ABK09794 ABK59653 AAQ73761
22 42 74 71 71	220 230 230 230 230 230 230 230 230 230	222222	22 22 22 22 23 23 23 23 23 23 23 23 23 2	H 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	11 11 12 12 12 12 12 12 12 12 12 12 12 1	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	8 6 7 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9

## ALIGNMENTS

RESULT 1

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Human; ds; single nucleotide polymorphism; SNP; P2X7-associated disorder; inflammation; immune disease; drug development; genetic marker; gene;
                                                                                                                                                                                  /*replace (253, C) /*tag= b /note= "Single nucleotide polymorphism"
                                                                                                                                                                                                                                                       /*tag= d
/note= "Single nucleotide polymorphism"
replace (760, G)
/*tag= e
/note= "Single nucleotide polymorphism"
                                                                                                                                                                                                                            /*tag= c
/note= "Single nucleotide polymorphism"
                                                                                                                                                                  /*tag= a
/product= "Human P2X7 protein"
                                                                                                                                             Location/Qualifiers
27..1814
                                                                                                                                                                                                                  replace (488, A)
                                                                Human P2X7 gene coding sequence.
                                                                                                                                                                                                                                                replace (489, T)
        펿.
      AAL43027 standard; DNA; 1853
                                                                                                                            Homo sapiens.
                                              08-AUG-2002
                                                                                                        P2X7 gene.
                           AAL43027;
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us-09-977-221-2.rng

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                                                       1 AAAACGCAGGGAGGCAGTGTCACCATGCCGGCCTGCAGCTGCAGCTGATGTTTTCC
                                                                                        AGTATGAGACGAACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAGTGGT
                                                                                                        181 AGCGGAAAGAGCCTGTCATCAGTTCTGTGCACCAAGGTGAAGGGGATAGCAGAGGTGA
                                                                                                                                                                                                             181 AGCGGAAAGAGCCTGTCATCAGTTCTGTGCACCAAGGTGAAGGGGATAGCAGAGGTGA
                                                                                                                                                                                                                                                                                      301 ACTACACOTTCCCTTTGCAGGGAACTCTTTCTTCGTGATGACAAACTTTCTCAAAACAG
                                                                                                                                                                                                                                                                                                   GTGTAGTRYATGAAGGGAACCAGAAGACCTGTGAAGTCTCTGCCTGGTGCCCCATCGAGG
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                                          1 AAAACGCAGGGAGGGAGGCTGTCACCATGCCGGCCTGCTGCAGTGTGTTTTCC
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                 0;
                   Indels
                 0
      ed. No. 0;
Mismatches
      Pred. No.
                 16;
      99.18;
                Matches 1837; Conservative
      Best Local Similarity
                                                                                        61
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                                                                                                                                                                                                             nucleotide polymorphism"
                                                                                                                                                                                                                                                                            .uoue= "Single nucleotide polymorphism" replace (1494, G)
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                                                                                                                                                                     /note= "Single nucleotide polymorphism"
replace (1324, T)
/*tag= k
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/note= "Single nucleotide polymorphism"
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T)
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/note= "Single nucleotide
replace (1096, G)
                                                                                                                                    /note= "Single nucleotide
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                                                            /note= "Single nucleotide
                                                                         replace (1068, A)
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                                      replace (853, A)
(835, A)
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replace (1448,
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2000US-244897P.
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06-APR-2001;
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1021 AGCTGGTTGTGTACATCGGCTCAACCCTCTCCTACTTCGGTCTGGCCCRCTGTGTTCATCG 1080

DB 24; Length 1853;

Score 1846.6;

99.78;

Query Match

Surprenant A;

ьj

m

us-09-977-221-2.rng

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AAGGCCAAGAGCAGCGGTTGTGTCTCCCGAGTATCCCACCCGCAGCACGCTCTGTTCCTCTG
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                                                                                                                                                     97US-0842079.
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                            sapiens
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                                                                 US6133434-A.
                                                                                                             17-0CT-2000
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                                                                                                                                                     GCTGCCGCTGGAGCATCCGGAAAGAGTTCCGAAGAGTGAAGGGCAGTACAGTGGCTTCA
                                                                    CTGCGATGGACTTCACAGATTTGTCCAGGCTGCCCCTGGCCCTCCATGACACACCCCCGA
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The present sequence is the coding sequence for human purinergic receptor P2X_7/P2Z. This sequence can be used to treat disorders of the nervous system, particularly diseases with a component of chronic inflammation, such as Alzheimer's diseases involving acute or chronic inflammation such as rheumatoid arthritis, amyloidosis, bacterial, viral and other microbial infections, disorders of the haematopoietic system and immune response such as autoimmune disorders, allergies and lymphoproliferative disorders, diseases involving apoptotic cell death, such as cardiac and cerebral isohaemia and microbial infections, particularly tuberculosis. The human P2X_7 gene has been localised to
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Mammalian purinergic receptor (P2X7) useful for screening for modulators which are useful for treating arthritic, respiratory disorders and neurodegenerative disorders, and to generate receptors
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99.1%; Pred. No. 0;
iive 16; Mismatches
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		Qy 1561 TGTTCAGGAAGCTGGTCCTGTCCAGACACGTCCTGC
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QY	CGGCCTGCTCTTGAACAGTCCGAAAACTTCACTGTCTCA 	Qy 1621 CCTTGCTKGCGCTGGATGTGGATTCCACCAACAGCCC Db 1621 CCTTGCTGGCGCTGGATGTGGATTCCACCAACAGCCC
λō tā	TCAAGAACAATATGGACTTCCCGGGCACAACTACACCAGGAAACATCCTGGCAGGTT	OY 1681 GCTACGCCACCTGCGCTTCGGCTCCCAGGACATGGC
a & a	TCAAGAACATATCUCACCOGCCACAACTACACCACGAGAACATCTGCCGGGTT  TAAACATCACTTGTACCTTCCACAGACTCCACACAGGGTCCCACATTTGCCACTAG	QY 1741 GCTGCCGCTGGAGGATCCGGAAAGAGTTTCCRAAGAG Db 1741 GCTGCCGCTGGAGGATCCGGAAAGAGTTTCCGAAAGAG
ස් දී	061 TAAACATCACTTGTACCTTCCACAAGACTCAGAATCCACAGTGTCCCATTTTCCGACTAG 720 721 GAGACATCTTCCGAGAAAACAGGCGATAATTTTTCAGATGKGGCAATTCAGGGCGGAATAA 780 721 GAGACATCTTCCGAGAACAGGCGATAATTTTTTCAGATGKGGCAATTCAGGAGGAATAA 780	QY 1801 AGAGTCCTTACTGAAGCCAGGCACCGTGGCTCACGTC
QY	TGGGCATTGAGATCTACTGGGACTGCAACCTAGACCGTTGGTTCCATCATTGCCRTCCCA	RESULT 3 AAF98411 ID AAF98411 standard; CDNA; 2168 BP.
Qy	841 AATACAGTTTCCRTCGCCTTGACGACAACGACCACCACCACGTGTACCCTGGCTACA 900	AAF98411;
Qy	901 ACTTCAGATACGCCAAGTACTACAAGGAAAACAATGTTGAGAAACGGACTCTGATAAAG 960 	Human cDNA clone C0390_1
da da	TCTTCGGGATCCGTTTTGACATCCTGGTTTTTGGCACGGAGGAAAATTTGACATTATCC	<pre>differentiation; immune system modulator; ti haemostatic; thrombolytic; anti-inflammatory haematopoiesis.</pre>
à ť	1021 AGCTGGTTGTGTACATCGGCTCAACCCTCTCCTACCTCGGCTCTGGCCTCTGGCTTCATCG 1080 1031 AGCTGGTTGTALIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OS Homo sapiens. XX VN WO200119988-A1.
3 & 4	ACTICCTCATCACACCTCACCTCTCCTCTCGGGTCTGGCGCTGTGTCCTCCTCGGTCTCGCACTTATTCCTCGGTGCACTTCTCTCTC	AA 22-MAR-2001. XX PF 14-SEP-2000; 2000WO-US25135.
G Z	ACTGCTCATCGACACTIACTCCACTACTCGCTCCCCCATATTTATCCCTGGTGCACACATACTCCTGGTGCACACAAACTACTACAGGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	XX PR 17-SEP-1999; 99US-0398829. XX Y GEMY ) GENETICS INST INC.
oy Oy	AGTGCTGTCAGCCCTG TGGAGCCAAAGCCGAC	XX PI Jacobs K, McCoy JM, LaVallie ER, Collins-Ra PI Merberg D, Treacy M, Bowman MR, Spaulding V XX
DP QY		WPI; 2001-244801/25. P-PSDB; AAB90689.
qq		PT Isolated nucleic acids encoding polypeptides, PT e.g. cytokine and cell proliferation/different PT immune system and hematopoiesis regulating acid
Q <sub>Y</sub>	1321 CTGYGATGGACTTCACAGATTTGTCCAGGCTGCCCCTGCCCTCCATGACACCCCCGA 1380 (  :	Disclosure, Page 419;
og .	1381 TTCCTGGACAACCAGAGAGATACRGCTGCTTAGAAAGGAGGGGGACTCCTAGATCCAGG 1440 	CC Human CDNA clones represented in AAF98374 - AA c proteins AAB90667 - AAB90750. The CDNA clones CC tissue trypes, and may be used in the preventic CC of diseases associated with inappropriate prof
Q7 Dp	1441 ATAGCCCYGTCTGGTGCCAGTGTGGAAGCTGCCTCCCATCTCAACTCCCTGAGRGCCACA 1500	CC polypeptides and nuclear acids may be used as CC cytckine and cell proliferation/differentiation of involved in modulation of the immune system. CC proteins, their agonists and/or antagonists e.
Qy Dp	1501 GGTGCCTGGAGGMGCTGCTGCCGGAAAAAGCCGGGGGCTGCATCACCACCTCAGAGC 1560 	CC regulating activity; tissue growth activity; a chemotactico/chemokinetic activity; haemostatico cotivity; receptor/ligand activity; anti-infile cc haematopoiesis activity; oadherin/tumour suppic cc tumour inhibition activity. Included in the in

SCAGTICCTCCTGCTCTACCAGGAGC 1620 CCGCCTGCGGCACTGTGCCTACAGGT 1680 GGTGACTTTGCCATCCTGCCCAGCT 1740 AGTGAAGGCAGTACAGTGGCTTCA 1800 - AAF98489 encode secreted ones are isolated from various antion, treatment and diagnosis protein expression. The as nutrients or to modulate lation activity and may also be am. The cDMA sequences, the exhibit haematopoiesis by; activin/inhibin activity; tatic and thrombolytic thin and thrombolytic inflammatory activity; suppressor activity; and/or he invention are probes modulator; proliferation;
lssue growth; chemotactic;
}; tumcour inhibition; ss; s, useful for modulating entiation activity, the activity -Racie LA, Evans C; V, Agostino MJ;

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GCCAAAGCCGACATTAAAGTATGTGTCCTTTGTGGATGAATCCCACATTAGGATGGTGAA
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                                                                                                                                                                                       QY
                                                                                                                                                                                                                                                                                                                                                                   δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This cDNA clone, designated CO390_1, codes for a novel human secreted protein (see AAM$8390). It was isolated from a human adult secreted protein (see AAM$8390). It was isolated from a human adult careful control in the clone is deposited in composite clone secreted proteins. The clone is deposited in composite clone is close and casigned to isolate CO390_1 DNA from the composite clone. Novel cDNA clones of acceptance may contain an Alu repetitive element. Novel cDNA clones (see AAV$9916-32) coding for human secreted proteins (see AAW$8580-90) are claimed. These can be used for recombinant production of the secreted proteins for analysis, characterisation, diagnostic or therapeutic use. They can also be used as tissue or mol. Wt. markers, for chromosome identification, to identify genetic disorders, to isolate new related DNA, as sources of primers for PCR, to generate may have many biological activities, es; cytokine, immunomodulator, harmonical activity, elementary and this activity activity harmonical activity activity and think activity and the manostatic or chemotactic or chemotactic or chemotactic activity, activit harmonical activity activit harmonical activity activity activit harmonical activity activity activity activity and the acceptance of activity activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haemostatic and thrombolytic activity, receptor/ligand activity, antitifiammatory, cadherin and tumour invasion suppressor activity, and tumour inhibition activity. The proteins can be expressed in vivo from DNA, introduced in gene therapy vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding secreted protein from human cells - useful, e.g. as immunomodulator, antitumour agent, promoters of tissue growth, haemostatic and thrombolytic agents etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1833.4; DB 19; Length 2169;
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                                                                                                                                                                                                                                                                                                                                                                                              JM,
                                                                                                                                                                                                                                                                                                                                                                                              McCoy
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              ER,
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                                           Location/Qualifiers
87..1874
/*tag= a
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Treacy M;
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98.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 98.4 Matches 1819; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           J, Jacobs F
Spaulding
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-261426/23.
P-PSDB; AAW58390.
sapiens
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                                                                                                                                                                                                                                                                                                                                                                                              Agostino MJ,
                                                                                                                                                                                     30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                   Racie LA,
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431 TAAAAAGGGATGGATGGACCCGCAGAGCAAAGGAATTCAGACCGGAAGGTGTGTAGTRYA 490
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                                                                                                   The present sequence is the coding sequence for rat purinergic receptor P2X_7/P2X. This sequence can be used to treat disorders of the nervous system, particularly diseases with a component of chronic inflammation, such as Alzheimer's disease, diseases involving acute or chronic inflammation such as rheumatoid arthritis, amyloidosis, bacterial, viral and other microbial infections, disorders of the heamatopoietic system and immune response such as autoimmune disorders, allergies and lymphopoliferative disorders, diseases involving apoptotic cell death, barticularly tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGTGAGCCTGTCGCCATGCCTGCTGCTGCTGCTGCAACGATGTCTTTCAGTATGAGAC
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     treating arthritic, respiratory disorders, and to generate receptors
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                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                            323;
                                                                                                                                                                                                                                                                                                                          Score 1282.4;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                            12; Mismatches
                                                                                                                                                                                                                                                                                         Sequence 3540 BP; 919 A; 958 C; 899 G; 764
   ich are useful for
neurodegenerative
                                                                       English.
                                                                                                                                                                                                                                                                                                                          69.2%;
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                                                                    40pp;
   modulators which are
                                      specific antibodies
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                                                                     1B;
                    disorders and
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                                                                     Claim 3;
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                                                                                                                                                                                                                                                                                                                       GCTKGCGCTGGATGTGGATTCCACCAACAGCGGGCTGCGGGCACTGTGCCTACAGGTGCTA 1684
                                                                                                                                                                                                                                                                                                                                          CGCCACCIGGCGCTTCGGCTCCCAGGACATGGCTGTTTGCCATCCTGCCCAGCTGCTG 1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGCTGGAGGATCCGGAAAGAGTTTCCRAAGAGTGAAGGGCAGTACAGTGGCTTCAAGAG 1804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1805 CCGCTGGAGGATCCGGAAAGAGTTTCCGAAGAGTGAAGGGCAGTACAGTGGCTTCAAGAG 1864
                                                                                                                                                                                    CCTGGAGGMGCTGTGCTGCCGGAAAAAGCCGGGGGCCTGCATCACCACCTCAGAGCTGTT 1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiarthritic; antibacterial; antiviral; antiallergic; cytostatic; carebroprotective; immunosuppressive; P2Z; purinergic receptor; nervous system disorder; chronic inflammation; Alzheimer's disease; rheumatoid arthritis; anyloidosis; bacterial; viral; microbial infection; haematopoietic system disorder; immune response; autoimmune disorder; allergy; lymphoproliferative disorder; cardiac; cerebral ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat; P2X_7; neuroprotective; nootropic; antiinflammatory; antirheumatic;
                                                                                                                                      GATGGACTTCACAGATTTGTCCAGGCTGCCCCTGGCCCTCCATGACACACCCCCGATTCC
                                                                                                                   CCCYGICTGGTGCCAGTGTGGAAGCTGCCTCCCATCTCAACTCCTGAGRGCCACAGGTG
                                                                                                                                                                                                                                                      CAGGAAGCTGGTCCTGTCCAGACGTCCTGCAGTTCCTCCTGCTCTACCAGGAGCCCTT
for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalian purinergic receptor (P2X7) useful for screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
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tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-1997;
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CCAGGAAATCGGAGAGAACTITACAGAGGTGGCAGTTCAGGGAGGAATCATGGGCATTGA 885

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                                                                                                      1246 GCCCTGTGCAGTGAATGAGTACTACTACAGAAGAAGTGTGAGCCCATCGTGGAGCCCAA
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GATCTACTGGGACTGCAACCTAGACCGTTGGTTCCATCACTGCCRTCCCAAATACAGTTT
           851 CCRTCGCCTTGACGACAAGACCACCAACGTGTCCTTGTACCCTGGCTACAACTTCAGATA
                                                                                          CGCCAAGTACTACAAGGAAAACAATGTTGAGAAACGGACTCTGATAAAAGTCTTCGGGAT
                                                                                                                                     971 CCGTTTTGACATCCTGGTTTTTGGCACCGGAGGAAATTTGACATTATCCAGCTGGTTGT
                                                                                                                                                   CGACASTTACTCCAGTAACTGCTGTCGCTCCCATATTTATCCCTGGTGCAAGTGCTGTCA
                                                                                                                                                                                                                                                    1186 CAACACGTATGCCAGTACCTGCTGCAGGTCACGTGTTTACCCCTCCTGTAAGTGCTGCAGA
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This nucleic acid sequence encodes the human purinoreceptor (HPURR), which has been shown to be similar to P2x purinoreceptors isolated from both human and rat. The nucleic acid was discovered from a spinal cord blat library (SCORMOTI) Incryte clone 555697, this was found by using a search for sequence alignments of amino acids. The consensus sequence was derived from the two overlapping and/or extended nucleic acid in the diagnosis, prevention, and treatment of disorders and diseases of the immune system, nervous system, cardiovascular, and of smooth muscle. For example, Alzheimer's, Huthinforn's, Parkinson's, Creutzfeldt-Jakob diseases, heart disease, troke, thrombosis and other coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231
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                                                        Purinoreceptor; HPURR; P2x; rat; spinal cord; immune system; nervous system; cardiovascular; smooth muscle; Alzheimer's; Huntington's Parkinson's; Creutzfeldt-Jakob disease; thrombosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 TITICCAGIATGAGACGAACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human purino-receptor and related nucleic acid - potentially useful for diagnosing or treating immune, nervous system, cardiovascular and smooth muscle diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 237; DB 19;
Pred. No. 1.5e-54;
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                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "HPURR protein"
                                                                                                                                                                                                                                                Location/Qualifiers
28..1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 51-55; 66pp; English.
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54.4%;
nucleic acid sequence.
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nes 574; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coleman R, Hillman JL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-1997;
                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                            WO9818916-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                        isolated polynucleotides, used to produce PX2 receptor polypeptides and identify potentially therapeutic compounds, encode a human P2X2 receptor polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 AGGCTACCAGGAACTGACTCCGTGGTCAGCTCCGTTACGACCAAGGTCAAGGCGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 AGTGGTTCTTCCACGTGATCATCTTTTCCTACG ---TTTGCTTTGCTCTGGTGACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 CAGAGGTGAAAGAGGAGATCGYGGAGAATGGAGTGAAGAAGTTGGTGCACAGTGTCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352 TCAAAACAGAAGGCCAAGAGCAGCGTTGTGTCCCGAGTATCCCACCCGCAGGACGCTCT
      Human; purinoreceptor; P2X2; P2X4; pain; nueroendocrine disease; auditory disease; vestibular disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36;
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                                                                                                                                                                                                                                                                                                                                   EB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.7%; Score 235.4; DB 22; Length ilarity 54.3%; Pred. No. 3.5e-54; Conservative 5; Mismatches 441; Indels
                                                                                                                                                                                                                                                                                                                                   Touma
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                                                                                                                                                                                                                                                                                                                                  Niforatos W,
                                                                                                                /*tag= a
/product= "purinoreceptor P2X4"
                                                                                                                                                                                                                                                                                                                                  Metzger RE,
                                                                              Location/Qualifiers 21..1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Fig 11; 40pp; English.
                                                                                                                                                                                                                                                     97US-0065822
98US-0137458
                                                                                                                                                                                                                        98US-0191608
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                                                                                                                                                                                                                                                                                                   (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 CAG----
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                                                                                                                                                                                                                                                                                                                                                  Van Biesen T;
                                                    Homo sapiens
                                                                                                                                                             US6242216-B1
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                                                                                                                                                                                                                     GTICCTCTGACCGAGGTTGTAAAAAGGGATGGATGGACCCGCAGAGCAAAGGAATTCAGA 471
                                                                                                                                                                                                                                                                                  CCGGAAGGIGIGIAGIRYAIGAAGGGAACCAGAAGACCIGIGAAGICICIGCCIGGIGCC 531
                                                                                                                                                                                                                                                                                                                                               CCATCGAGGCAGTGGAAGAGGCCCCCGGGCCTGCTCTTGAACAGTGCCGAAAACTTCA 591
                                                                                                                                                                                                                                                                                                                                                                          CGGTGGAGGATGACACACGTGCCACAACCTGCTTTTTTAAAGGCTGCAGAAAACTTCA 583
                                                                                                                                                                                                                                                                                                                                                                                                          CIGIGCICATCAAGAACAATAICGACIICCCCGGCCACAACIACACCGAGGAAACAICC 651
182 AGGCTACCAGGAAACTGACTCCGTGGTCAGCTCCGTTACGACCAAGGTCAAGGGCGTGG 241
                                 CAGAGGTGAAAGAGAGATCGYGGAGAATGGAGTGAAGAAGTTGGTGCACAGTGTCTTTG 291
                                                              CTGTGACCAACACTTCTAAACTTGGATTCCGGATGTGGGCGGATTATGTGATAC
                                                                                            464 CAGGCAGGTGCGTAGCTTTCAACGGGTCCGTCAAGACGTGTGAGGTGGCGGCCTGGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  824 CCGCCTCCTCTGCTTGCCCAGGTACTCCTTCCGCCGCCTCGATACACGGGACGTTGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               937 TIGAGAAACGGACICIGATAAAAGICIICGGGAICCGIITIIGACAICCIGGITITIIGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGGAGGAAAATTTGACATTATCCAGCTGGTTGTGTACATCGGCTCAACCCTCTCCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of a human purinoreceptor P2X4.
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                                                                                                                           302 CAG----
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This cDNA encodes a human brain P2X-1 receptor polypeptide. The P2X receptor splice variants (P2X-1, P2X-2 and P2X-3 isoforms) can be recombinantly expressed by a host cell genetically neglneered with a recombinantly expressed by a host cell genetically neglneered with a vector containing the encoding nucleic acids. The receptors can be used to escreen for their antagonists. The products can be used to identify to screen for their antagonists. The products can be used to identify agents which modulate the activity of the receptors for use in clinical conditions such as brain stroke, brain or spinal cord traumas, infection and inflammation, cognitive disorders, epilepsy, affective and mood a disorders in general, including depression, various movement disorders including Parkinson's disease, Huntingtons Chorea and Schizophrenia, as well as those conditions that are associated with the development of chronic or acute forms of path, or cardiac anoxia. The products can also be used for detection, production of antibodies and production of transgenic animals as models for mutation and structure/activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTTCCAGTATGAGACGAACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTA 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  472 CCGGAAGGTGTGTAGTRYATGAAGGGAACCAGAAGACCTGTGAAGTCTCTGCCTGGTGCC
                                                                                                                                                                                                                                                                                    DNA encoding human brain P2x receptors - used to develop products for treating, e.g. brain or spinal cord traumas, infection, inflammation and mood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 235.4; DB 18; Length 1759;
Pred. No. 4.2e-54;
5; Mismatches 441; Indels 36;
                                                                                                                                                                 MCHALE MT, Tomlinson WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1759 BP; 402 A; 496 C; 480 G; 381 T; 0 other;
                                                                                                                                                            Carpenter DJ, Livingstone CD,
                                                                                                 HUMAN GENOME SCI INC.
SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Fig 1; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 54.3%;
Matches 573; Conservative
                                                          96WO-GB01034
                 96WO-GB01034
                                                                                                                                                                                                                         WPI; 1997-549726/50.
P-PSDB; AAW47066.
                 30-APR-1996;
                                                        30-APR-1996;
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                                                                                                                       CAGGCAGGTGCGTAGCTTTCAACGGGTCCGTCAAGACGTGTGAGGTGGCGGCCTGGTGCCC
                                                                                                                                                                                                                CGGTGGAGGATGACACACACGCACAACCTGCTTTTTTAAAGGCTGCAGAAAACTTCA
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                                                    397 GIRARATCAGATGCCAGCTGTACTGCCGGCTCTGCCGGCACCCACACGGAGTCTCAA
                                                                                                                                                                              CCATCGAGGCAGTGGAAGAGGCCCCCGGCCTGCTCTTGAACAGTGCCGAAAACTTCA
                                                                                                                                                                                                                                                              CTGTGCTCATCAAGAACAATATCGACTTCCCCGGCCACAACTACACCACGAGAAACATCC
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                                                                                               CCGGAAGGTGTGTAGTRYATGAAGGGAACCAGAAGACCTGTGAAGTCTCTGCCTGGTGCC
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14.1180
74.729 / Product - "Human brain P2x-1 receptor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human brain P2X-1 receptor encoding cDNA.
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                                                                                                                                                                                                                                  Rat P2x clone 3 (AAF133853) codes for the superior cervical ganglion P2x receptor (AAF04216), a ligand-gated ion channel that opens upon binding of extracellular AFP. It was isolated by screening a rat testis cDNA bank with a probe obtd. by PCR amplification of testis cDNA using primers (see also AAF13857-58) based on the rat was deferens P2x receptor cDNA (AAF13852). A rat dorsal ganglion P2x receptor cDNA (AAF13854) was similarly isolated, and a human homologue (AAF13855) was also identified. The cDNA can be used to produce recombinant P2x receptors in host (e.g. COS) cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 TITICCAGTATGAGACGAACAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                477 GTAATTCAGACGCCGACTGCACCCCGGGCTCCGTGGACACCCCACAGCAGTGGAGTTGCGA
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                                                                                                                     DNA encoding ATP P2x receptors of the purinoceptor family - for
                                                                                                                                        screening cpds. useful in treating epilepsy, cognition, emesis, pain, asthma, peripheral vascular disease, hypertension, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17; Length 1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1997 BP; 470 A; 523 C; 542 G; 462 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 234.6; DB 1
Pred. No. 7.4e-54;
                                                                                                                                                                                                 Claim 1; Fig 2; 82pp; English
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55.5%;
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                                                          WPI; 1996-030561/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                            .-----TGTACCTTCCACAGACTCAGAATCCAC 699
                                     TICCCAACATCACCACTACTTACCTCAAGTCGTGCATTTATGATGCTAAAACAGATCCCT
                                                                                                                                                                                                                                                       700 AGIGICCCATITICCGACIAGGAGACAICIICCGAGAAACAGGCGAIAAITITICAGAIG
                                                                                                                                                                                                                                                                                                                                       KGGCAATTCAGGGCGGAATAATGGGCATTGAGATCTACTGGGACTGCAACCTAGACCGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          870 ACAACGIATCICCIGGCIACAATITCAGGITTGCCAAGIACTACAGAGACCIGGCIGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  937 ITGAGAAACGGACTCTGATAAAGTCTTCGGGATCCGTTTTGACATCCTGGTTTTTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGGAGGAAAATTTGACATTATCCAGCTGGTTGTGTACATCGGCTCAACCCTCTCCTACT
            CCATCGAGGCAGTGGAAGAGGCCCCCCGGCCTGCTCTTGAACAGTGCCGAAAACTTCA
                                                                                          CTGTGCTCATCAAGAACAATATCGACTTCCCCGGCCACAACTACACCACGAGAAACATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP P2x receptor; purinoceptor; ligand-gated ion channel; agonist; antagonist; epilopsy; cognition; emesis; pain; asthma; peripheral vascular disease; hypertension; irritable bowel syndrom premature ejaculation; cystitis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat superior cervical ganglion P2x receptor cDNA clone 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGGTCTGGCCRCTGTGTTCATCGACTTCCTCATC 1091
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are potential therapeutic agents in several disorders including central nervous system or peripheral nervous system conditions, e.g., epilepsy, pain, depression, neurodegenerative disorders of the skeletal muscle such as neuromuscular diseases, disorders of the reproductive system, asthma, peripheral vascular disease, hypertension, immune system disorders, irritable bowel disorder, premature ejacularion, cystic fibrosis and chronic bronchits. P2Y purinoreceptors mediate the activity of extracellular nucleotide triphosphates to regulate chloride secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTTCGAGTACGACACGCCGCGCATCGTGCTCATCCGCAGCCGCAAAGTGGGGGCTCATGA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 ATGTGGCGGATTATGTGATACCAGCTCAGGAGAAACTCCCTCTTCGTCATGACCAACG 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 697 CACAGIGICCCATITICCGACTAGGAGACATCITCCGAGAAACAGGCGATAATITITCAG 756
                                                                                      The present sequence is human P2X4 receptor DNA containing its open reading frame with EcoRI restriction used for subcloning. P2X receptors are ligand-grated ion ribanels while P2Y receptors operate generally through a G-protein coupled system. P2X purinoreceptor drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                      55 ITTTCCAGTATGAGACGAACAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCTGTACCAGCGGAAAGAGCCTGTCATCAGTTCTGTGCACACCAAGGTGAAGGGGGATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 AGGGCTACCAGGAAACTGACTCCGTGGTCAGCTCCGTTACGACCAAGGTCAAGGCGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 ACACCGCAGACTACACCTTCC---CTTTGCAGGGGAACTCTTTCTTCGTGATGACAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469 AGACCGGAAGGTGTGTAGTRYATGAAGGGAACCAGAAGACCTGTGAAGTCTCTGCCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  529 GCCCCATCGAGGCAGTGGAAGAGGCCCCCGGCCTGCTCTTGAACAGTGCCGAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCACTGTGCTCATCAAGAACAATATCGACTTCCCCGGCCACAACTACACCACGAGAAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         635 TCCTTCCCAACATCACCACTACCTCAAGTCGTGCATTTATGATGCTAAAACAGATC
   polypeptide useful for identifying potentially therapeutic compounds that modulate or otherwise interact with P2x containing receptors \,
                                                                                                                                                                                                                                                                                                                                                                  Score 233.8; DB 22; Length 1207;
Pred. No. 9.5e-54;
4; Mismatches 432; Indels 41;
                                                                                                                                                                                                                                                                                                                                   Sequence 1207 BP; 285 A; 335 C; 320 G; 266 T; 1 other;
                                                      English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        649 TCCTGCCAGGTTTAAACATCACT-
                                                                                                                                                                                                                                                                                                                                                                   12.6%;
54.9%;
                                                                                                                                                                                                                                                                                                  human airway epithelia.
                                                        53pp;
                                                                                                                                                                                                                                                                                                                                                                   Query Match 12.6
Best Local Similarity 54.9
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                                                        Example 11; Fig 10;
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                                                                                                                                                                                                            CCGGAGGAAAATTTGACATTATCCAGCTGGTTGTGTACATCGGCTCAACCCTCTCCTACT 1056
                                                                                                                                                                                                                                                                                                                                                                1077 AGCCIGGGAAGTITGACATCATCCTACCATGATCAACGTTGGCCTCTGGCCTTGGCGCTCC 1136
                                                                                                                                                                                                                                                                966
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                     836
                                                                                                                     GGTTCCATCACTGCCRTCCCAAATACAGTTTCCRTCGCCTTGACGACAAGACCAACG 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; purinergic receptor; P2X4; antidepressant; vulnerary; hypotensive; anticorvulsant; antilnflammatory; therapy; nervous system disorder; epilepsy, pain; depression; neurodegenerative disorder; cystic fibrosis; irritable bowel disorder; reproductive system disorder; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peripheral vascular disease; immune system disorder; chronic bronchitis; premature ejaculation; asthma; neuromuscular disease; ds.
CGGCCTCCCTTTGCCTGCCCAGATATTCCTTCCGGCGCTGGACACCCGGGACCTGGAAC
                                                                                                                                                                                                                                                                                    1017 AAGAGCAGCACACTCACCAAGGCGTACGGCATCCGCTTTGACATCATCGTGTTTGGAA
                                                  KGGCAATTCAGGGCGGAATAATGGGCATTGAGATCTACTGGGACTGCAACCTAGACCGTT
                                                                                                                                                                                           TGTCCTTGTACCCTGGCTACAACTTCAGATACGCCAAGTACTACAAGGA---AAACAATG
                                                                                                                                                                                                                                                           937 TTGAGAAACGGACTCTGATAAAGTCTTCGGGATCCGTTTTGACATCCTGGTTTTTGGCA
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"Represented in the specification as
                                                                                                                                                                                                                                                                                                                                                                                                  TCGGTCTGGCCRCTGTGTTCATCGACTTCCTCATC 1091
                                                                                                                                                                                                                                                                                                                                                                                                                  TCGGGGTGGCGACGGTGCTCTGTGACGTCT171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Human P2X4 receptor"
263
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98US-0008185.
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16-JAN-1998;
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1059 TCCCCACTATGATCAACATCGGCTCTGGCCTGGCACTGCTAGGCATGGCGACCGTGCTGT 1118
                                                                                                                                                            Best Local Similarity
Matches 453; Conserv
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                                                                                935 GCAACGAGGAGGCCACGCTCATCAAGGCCTATGGCATCCGCTTCGACATCATTGTGTTTG 994
           GTTGGTTCCATCACTGCCRTCCCAAATACAGTTTCCRTCGCCTTGACGACAAGACCACCA
ATGKGGCAATTCAGGGCGGAATAATGGGCATTGAGATCTACTGGGACTGCAACCTAGACC
                                                                     ACGEGICCTEGIACCCEGGCIACAACTECAGATACGCCAAGTACTACAAGGAAAACAATG
                                                                                                        ---TTGAGAAACGGACTCTGATAAAAGTCTTCGGGATCCGTTTTGACATCCTGGTTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This cDNA encodes a human brain P2X-2 receptor polypeptide. The P2X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding human brain P2x receptors - used to develop products treating, e.g. brain or spinal cord traumas, infection,
                                                                                                                                                                                                                                                                                                                                                                                                                /note= "48 base pair insertion to P2X-1 receptor generates P2X-2 receptor"
                                                                                                                                                                                                                                                                                                                  treatment; trauma; spinal cord; infection; mood disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tomlinson WJ;
                                                                                                                                                                                                                                                                                                                                                                                        "Human brain P2X-2 receptor"
                                                                                                                                                                                       1054 ACTICGGICTGGCCRCTGTGTTCATCGACTTCCTCATC 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carpenter DJ, Livingstone CD, MCHALE MT,
                                                                                                                                                                                                                                                                                               P2X-2 receptor encoding cDNA
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14..1228
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SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Fig 2; 31pp; English
                                                                                                                                                                                                                                           AAV09308 standard; DNA; 1807
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P-PSDB; AAW47067.
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                                                                                                                                                                                                                                                                                               brain
                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                  Brain;
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receptor splice variants (P2X-1, P2X-2 and P2X-3 isoforms) can be recombinantly expressed by a host cell genetically engineered with a vector containing the encoding nucleic acids. The receptors can be used to screen for their antagonists. The products can be used to identify agents which modulate the activity of the receptors for use in clinical conditions such as brain stroke, brain or spinal cord traumas, infection and inflammation, cognitive disorders, epilepsy, affective and mood disorders in general, including depression, various movement disorders including Parkinson's disease, Huntingtons Chorae and schizophrenia, as vell as those conditions that are associated with the development of chronic or acute forms of pain, or cardiac anoxia. The products can also be used for detection, production of antibodies and production of transgenic animals as models for mutation and structure/activity relationship evaluations as well as in drug screening. 1017 TCCAGCTGGTTGTGTACATCGGCTCAACCCTCTCCTACTTCGGTCTGGCCRCTGTGTTCA 1077 869 720 758 780 840 878 900 957 432 AGGCCIATGGCATCCGCTTCGACATCATTGTGTTTGGGAAGGCAGGGAAATTTGACATCA ------TGTACCTTCCACAAGACTCAGAATCCACAGTGTCCCATTTTCCGACTAG AAGTCTTCGGGATCCGTTTTGACATCCTGGTTTTTGGCACCGGAGGAAATTTGACATTA 313 CTTTGCAGGGGAACTCTTTCTTCGTGATGACAAACTTTCTCAAAACAGAAGGCCAAGAGC 373 AGCGGTTGTGTCCCCGAGTATCCCACCCGCAGGACGCTCTGTTCCTCTGACCGAGGTTGTA 433 AAAAGGGATGGATGGACCCGCAGAGCAAAGGAATTCAGACCGGAAGGTGTGTAGTRYATG 579 Teccacaaccrectritraaagecrecagaaaacricacretrirgerraagaacaaca 613 TCGACTTCCCCGGCCACAACTACACCACGAGAAACATCCTGCCAGGTTTAAACATCACT-699 ACCICAAGICGIGCAITIAIGAIGCIAAAACAGAICCCIICIGCCCCAIAIICCGICIIG GAGACATCTTCCGAGAAACAGGCGATAATTTTTCAGATGKGGCAATTCAGGGCGGAATAA 781 TGGGCATTGAGATCTACTGGGACTGCAACCTAGACCGTTGGTTCCATCACTGCCRTCCCA 841 AATACAGITICCRICGCCTIGACGACAAGACCAACGAGGTGTCCTIGTACCCTGGCTACA ACTICAGATACGCCAAGTACTACAAGGAAAACAATG---TTGAGAAACGGACTCTGATAA ATTICAGGTTTGCCAAGTACTACAGAGACCTGGCTGGCAACGAGCAGCGCACGCTCATCA 399 AGGGCCTGTGCCCCGAGATTCCAGATGCGACCACTGTGTGTAAATCAGATGCCAGCTGTA AAGGGAACCAGAAGACCTGTGAAGTCTCTGCCTGGTGCCCCATCGAGGCAGTGGAAGAGG CCCCCCGGCCTGCTCTTGAACAGTGCCGAAAACTTCACTGTGCTCATCAAGAACAATA DB 18; Length 1807; Sequence 1807 BP; 415 A; 507 C; 493 G; 392 T; 0 other; 322; .6e-52; 4; Mismatches Score 227.2; Pred No 7 6 Pred. No. 12.3%; 57.1%; Conservative

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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by MR chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of GS is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in GS: (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially CA or an agent capable of modulating GCA or an inflammation (especially CA coronic) in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially CA chronic) in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from GS, where the level of expression in a sample of the tissue of gene(s) from GS, where
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 viral infection; parasitic infection; protozcal infection; fundal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonepiritis; asthma thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cDNA differentially expressed in granulocytic cells #909.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              granulocytic cell; DNA chip; bacterial infection;
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                                                                                                                                                                                                                                                                                                                                             ABK84338 standard; cDNA; 2633
                                                                                              1119 GTGACATCATAGTC 1132
1078 TCGACTTCCTCATC 1091
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reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease, also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and MS is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 24; Length 2633;
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                                                                                                                                                                                                                                     The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (1) a signature gene set, where (1) comprises a sequence (S) selected from 847 sequences (given in ABLG1664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid,
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Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 203.8; DB 24; Length 2633; Pred. No. 2.5e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2633 BP; 582 A; 804 C; 701 G; 546 T; 0 other;
                                                                                                                                                                     Claim 1; SEQ ID 8354; 44pp; English.
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54.8%;
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963 GACTGGCACGTACGGCACTGCAGACCCATCTATGAGTTCCATGGGCTGTACGAAGAGAAAA 1022
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                                     464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           843 CACCCCCTGTGCCCAGTCTTCCAGCTTGGCTACGTGGTGCAAGAGTCAGGGCCAGAACTTC 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     753 TCAGATGKGCCAATTCAGGGCGGAATAATGGGCATTGAGATCTACTGGGACTGCAACCTA 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   903 AGCACCCTGGCTGAGAAGGGTGGAGTGGTTGGCATCACCATGGACTGGCACTGTGACCTG 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   813 GACCGITGGITCCAFCACIGCCRICCCAAAIACAGITTCCRICGCCTTGACGACAAGACC 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour; gene therapy; ss.
                   662
                                                                                                                                                                                                                                                                      584
                                                                                                                                                                                                                                                                                                  663 regrececerceaegregargaceaecarecececerecerrereceaeaegeceae 722
                                                                                                             483 ACCAATITCATCGTGACCCCGAAGCAGACTCAAGGCTACTGCGCAGAGCACCCCAGAAGGG
                                                                                                                                            465 ATTCAGACCGGAAGGTGTGTAGTRYATGAAGGGAACCAGAAGACCTGTGAAGTCTCTGCC
                                                                                                                                                                                                                             TGGTGCCCCATCGAGGCAGTGGAAGAGGCCCCCCCGGCCTGCTCTTGAACAGTGCCGAA
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                                                                                                                                                                                                                                                                                                                                                                                             645 AACAICCIGCCAGGITIAAA------CAICACTIGIACCIICCACAAGACICAG
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                                                                               345 AACTITCTCAAAACAGAAGGCCAAGAGGCAGCGGTTGTGTCCCCAGTATCCCACCGCAGG
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                                                  -----ATCICICCCCAGGCIICAACIICAGGIIIGCCAGGCACIIIGIGGAGAAC 1096
                                                                                         GGCACCGGAGGAAAATTTGACATTATCCAGCTGGTTGTACATCGGCTCAACCCTCTCC 1052
                                                                                                                        1157 GGCAAGGCCGGGAAGTTTGACATCATCCTACAATGACCACCATCGGCTCTGGAATTGGC 1216
                              933 AATGTTGAGAAACGGACTCTGATAAAGTCTTCGGGATCCGTTTTGACATCCTGGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                        ATP P2x receptor; purinoceptor; ligand-gated ion channel; agonist; antagonist; palinepsy; cognition; emesis; pain; asthma; peripheral vascular disease; hypertension; irritable bowel syndrome; premature ejaculation; cystitis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A cDNA clone (AAT33855) codes for the human urinary bladder P2x receptor (AAW04218), a ligand-gated ion channel that opens upon binding of extracellular ATP. It was isolated from a bladder CDNA library using a rat smooth muscle P2x receptor probe. Rat was deferens, superior cervical ganglion and dorsal root ganglion P2x receptor CDNAs (AAT3852-54) have also been isolated. These CDNAs can be used to produce recombinant P2x receptors in host, esp. mammalian, cells for use in screening (ant)agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding ATP P2x receptors of the purinoceptor family - for screening cpds. useful in treating epilepsy, cognition, emesis, pain, asthma, peripheral vascular disease, hypertension, etc.
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Pred. No. 2.5e-45;
5; Mismatches 342; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2643 BP; 607 A; 794 C; 701 G; 541 T; 0 other;
                                                                                                                                                       1053 TACTTCGGTCTGGCCRCTGTTCATCGACTTCCT 1087
                                                                                                                                                                         1217 ATCTTTGGGGTGGCCACAGTTCTCTGTGACCTGCT 1251
                                                                                                                                                                                                                                                                                                                                                            Human urinary bladder P2x receptor cDNA.
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174..1373
/*tag= a
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54.8%;
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94GB-0010664.
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1046 A---
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27-MAY-1994;
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Homo sapiens,

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636 ACCACGAGAAACATCCTGCCAGGTTTAAACATCACTTGTACCTTCCACAAGACTCAGAAT 695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein tare predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, haematopoiesis regulating activity, tresque growth activity, haematopoiesis regulating activity, receptor/ligand activity, anti-inflammatory activity. Cadherin/tumour invasion suppressor activity, tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                             New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.6%; Score 196.4; DB 20; Length 294; Best Local Similarity 98.5%; Pred. No. 9e-44; Matches 197; Conservative 1; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                             Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
Racie LA, Spaulding V, Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 294 BP; 81 A; 72 C; 68 G; 73 T; 0 other;
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                                        WO9845436-A2
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US-08-842-079-16

US-08-12-671-2

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US-09-363-745-6

US-09-363-745-10

US-09-363-745-10

US-08-750-134A-4

US-09-363-745-4

US-09-191-186-13

US-09-191-186-13

US-09-191-608-14

US-09-191-608-14

US-09-191-608-15

US-09-191-608-15

US-09-191-608-15

US-09-191-608-15

US-09-191-608-16

US-09-191-608-15

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US-09-191-608-16

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US-09-191-608-16

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US-09-191-608-16

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US-09-191-608-16

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US-09-191-608-8

US-09-191-608-8
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Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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99.6%; Score 1845; DB 3;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1836; Conservative 16; Mismatches 1;
US-09-978-197-3
US-08-232-463-14
US-09-191-608-1
US-09-191-608-1
US-08-256-496-1
US-08-266-496-1
US-08-266-496-1
US-08-105-812-3
US-08-105-812-3
US-08-105-812-3
US-08-105-481-493-1
US-08-484-494-1
US-08-249-003-1
US-08-249-003-1
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US-08-484-494-6
US-08-484-494-6
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Patent No. 6133434
GENERAL INFORMATION
APPLICANT: BUELL, GARY N.
APPLICANT: SURPRENANT, ANNMARIE
APPLICANT: KAWASHITA, ERIC
TITLE OF INVENTION: A PURINBEGIC RECEPTOR
FILE REFERENCE: 1430-160
CURRENT APPLICATION NUMBER: US/08/342,079
CURRENT FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: Nucleic Acids Encoding a Functional
TITLE OF INVENTION: Human Purinoreceptor P2X2 and P2X4 And Methods Of Production
TITLE OF INVENTION: Human Purinoreceptor P2X2 and P2X4 And Methods Of Production
TITLE OF INVENTION: And Use Thereof
FILE REPERBANCE: 6344.US. 11
CURRENT APPLICATION NUMBER: US/09/191,608
CURRENT FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
                CCGGAGGAAAATTTGACATTATCCAGCTGGTJGTGTACATCGGCTCAACCCTCTCCTACT 1056
                               CCATCGAGGCAGTGGAAGAGGCCCCCGGCCTGCTCTTGAACAGTGCCGAAAACTTCA 591
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; Mismatches 441;
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                                                                                                                                                                  Sequence 21, Application US/09191608; Patent No. 6242216; GENERAL INFORMATION:
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                                                                                                                                                                                                            APPLICANT: Lynch, Kevin J.
APPLICANT: Burgard, Edward C.
APPLICANT: Metager. Randy E.
APPLICANT: Niforatos, Wende
APPLICANT: Touma, Edward B.
APPLICANT: Yan Biesen, T.
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al Similarity 54.3%;
573; Conservative
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Pred. No. 1.2e-59;
5; Mismatches 440; Indels
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                                                                                    12.8%;
54.4%;
                                                                                                   Similarity 54.4
4; Conservative
                                            CONSENSUS
             IMMEDIATE SOURCE:
LIBRARY:
MOLECULE TYPE:
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Best Local Similarity 55.5
Matches 585; Conservative
LENGTH: 1997 base pai
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                              652 IGCCAGGITTAAACATCACT------TGTACCTTCCACAAGACTCAGAATCCAC
                                                                                                        637 ITCCCAACATCACCACTACTTACCTCAAGTCGTGCATTTATGATGCTAAAACAGATCCCT
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                          CTGTGCTCATCAAGAACAATATCGACTTCCCCGGCCACAACTACACCACGAGAAACATCC
                                                   577 CTCTTTTGGTTAAGAACAACATCTGGTATCCCCAAATTTAATTTCAGCAAGAATATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VALERA, SOLEDAD
APPLICANT: BUELL, GARY
TITLE OF INVENTION: P2x RECEPTORS (PURINOCEPTOR FAMILY)
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1057 TCGSTCTGCCRCTGTTCATCGACTTCCTCATC 1091
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APPLICATION NUMBER: US/08/750,134A FILING DATE: 22-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08750134A Patent No. 5985603 GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4006
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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NAME: CRAWFORD, ARTHUR C.
REGISTRATION NUMBER: 25,3
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STATE: VIRGINIA
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                      Gaps
                                                                   36;
         Length 1997;
                                                                   Indels
Score 234.6; DB 2;
Pred. No. 6.8e-59;
5; Mismatches 429;
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1077 AGGCTGGGAAGTTTGACATCATCCTACCATGATCAACGTTGGCTTGGCGTTGGCGTCC 1136
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----ACCTCTCAGCTTGGATTCCGGATCTGGGACGTGGCGGACTATG 368
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                                                                                                                         352 TCAAAACAGAAGGCCAAGGAGCGGTTGTGTCCCGAGTATCCCACCCGCAGGACGCTCT
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Patent No. 5885603
GENERAL INFORMATION:
APPLICANT: VALERA, SOLEDAD
APPLICANT: BUELL, GARY
TITLE OF INFORTION: P2x RECEPTORS (P
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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    315 CTGTGACCAAC-
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US-08-750-134A-10
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                                                                        1077 AGGCTGGGAAGTTTGACATCATCCTACCATGATCAACGTTGGCTCTGGCTTGGCGTCC 1136
    1017 AAGAGCAGCGCACACTCACCAAGGCGTACGGCATCCGCTTTGACATCATCGTGTTTGGAA 1076
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                                            CCGGAGGAAAATTTGACATTATCCAGCTGGTTGTGTACATCGGCTCAACCCTCTCCTACT 1056
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                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: VALERA, SOLEDAD
APPLICANT: BUELL, GRY
TITLE OF INVENTION: P2x RECEPTORS (PURINOCEPTOR FAMILY)
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFRWHING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.7%; Score 234.6; DB 4;
55.5%; Pred. No. 6,8e-59;
ive 5; Mismatches 429;
                                                                                                                                               TCGGTCTGGCCRCTGTGTTCATCGACTTCCTCATC 1091
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REFERENCE/DOCKET NUMBER: 1430-116
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/09/363,745
                                                                                                                                                                                                                                                                                                                                                                                                                                E: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/750,134
FILING DATE:
                                                                                                                                                                                                                                                                    Sequence 6, Application US/09363745 Patent No. 6194162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (703) 816-4006
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 6:
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRAWFORD, ARTHUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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Matches 585; Conservative
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STREET: 1100 NOR:
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 22201-4714
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CLASSIFICATION:
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                                                                                                                                                                                                                              RESULT 6
US-09-363-745-6
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                                                                               1074 GGGACCAACTACCGTCACCTCTTCAAGGTGTTTGGGATTCGCTTTGACATCCTGGTGGAC 1133
                                                                                                                       GGCACCGGAGGAAATTTGACATTATCCAGCTGGTTGTGTACATCGGCTCAACCCTCTCC 1052
                                                                                                                                          933 AATGTIGAGAAACGGACTCTGAIAAAAGTCTTCGGGATCCGTITTGACAICCTGGTTTTI 992
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Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                              1194 ATCTTTGGGGTGCCACAGTTCTCTGTGACCTGCT 1228
                                                                                                                                                                                                      1053 TACTTCGGTCTGGCCRCTGTGTTCATCGACTTCCT 1087
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Pred. No. 9.4e-50;
5; Mismatches 342;
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APPLICATION NUMBER: US/09/363,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/09363745
Patent No. 6194162
GENERAL INFORMATION:
APPLICANT: VALERA, SOLEDAD
APPLICANT: BUELL, GARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/750,134 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE SOFTWARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPENDES: (703) 816-4006
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 10:
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LENGTH: 2643 base pairs
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Best Local Similarity 54.8'
Matches 447; Conservative
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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US-09-363-745-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACTTCACTGTGCTCATCAAGAACAATATCGACTTCCCCGGGCCACAACTACACCACGAGA 644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2643;
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                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/750,134A
ELING DATE: 22-3M-1997
CLASSIFICATION: 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches 342;
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Pred. No. 9.4e-50;
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                                                                                                                                                                                                               ATTORNEZ/AGENT INFOGRATION:
NAME: CRAWPORD, ARTHUR C.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET WUMBER: 1430-
TELEPHONE: (703) 816-4006
TELEPRA: (703) 816-4100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2643 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.0%;
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                 ZIP: 22201-4714
COMPUTER READABLE FORM:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                            Score 159.6; DB 2;
Pred. No. 7.8e-37;
6; Mismatches 395;
                         REGISTRATION NUMBER: 25,327
REFERENCE/DOKET NUMBER: 1430-116
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 816-4006
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              ; CLONE: rat P2x from vas deferens US-08-750-134A-4
                                                                                                                                                                                                                                                                                                                                                          8.6%;
          CRAWFORD, ARTHUR C.
                                                                                                                                                                    LENGTH: 1837 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
Matches 434; Conserv
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                                                                                                                         TGGTGCCCCATCGAGGCAGTGGAAGAGGCCCCCCGGCCTGCTCTTGAACAGTGCCGAA 584
                                                                                                                                                                                                                                               723 AACTICACICITITCAICAAGAACAGCAICAGCITICCACGCIICAAGGICAACAGGGGG 782
                                                                                                                                                                                                      585 AACTICACTGTGCTCATCAAGAACAATATCGACTTCCCCGGGCCACAACTACACCACGAGA
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543 GGCATATGCAAGGAAGACAGTGGCTGTACCCCTGGGAAGGCCCAAGAGGAAGGCCCAAGGC
                                          ATTCAGACCGGAAGGTGTAGTRYATGAAGGGAACCAGAAGACCTGTGAAGTCTCTGCC
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                                                                                 ATCCGCACGGCCAAGTGTGTGGCCTTCAACGACATGTGAAGACGTGTGAGATCTTTGGC
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APPLICANT: VALERA, SOLEDAD
APPLICANT: BUELL, GARY
TITLE OF INVENTION: P2x RECEPTORS (PURINOCEPTOR FAMILY)
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: US/08/750,134A
FILING DATE: 22-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08750134A Patent No. 5985603
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US-08-750-134A-4
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TITLE OF INVENTION: Nucleic Acids Encoding A Functional
TITLE OF INVENTION: Human Purinoreceptor P2X3 and P2X6 And Methods Of Production
TITLE OF INVENTION: Human Purinoreceptor P2X3 and P2X6 And Methods Of Production
TITLE OF INVENTION: And Use Thereof
FILE REFERENCE: 6293.03.Pl
CURRENT APPLICATION NUMBER: US/09/191,136B
CURRENT FILING DATE: 1998-01-16
EARLIER PILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: US 09/008,185
EARLIER APPLICATION NUMBER: US 60/071,298
EARLIER APPLICATION NUMBER: US 60/071,669
EARLIER RELING DATE: 1998-01-16
SARLIER RELING DATE: 1998-01-16
SARLIER RELING DATE: 1998-01-16
SARLIER RELING DATE: 1998-01-16
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                             604 AGAACAATATCGACTTCCCCGGCCACAACTACACCACGAGAAACATCCTGCCAGGTTTAA 663
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    598 GTGGCTGCACTCCAGGAAAAGCAGAAAGGAAAGCCCAAGGTATTCGCACAGGCAACTGTG 657
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APPLICANT: Abbott Laboratories
APPLICANT: Lynch, Kevin J.
APPLICANT: BUTGATG, Edward C.
APPLICANT: Van Biesen, T.
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                                                                                                                                                                                                                                                                                                                    APPLICANT: VALERA, SOLEDAD
APPLICANT: BUELL, GARY
TITLE OF INVENTION: P2x RECEPTORS (PURINCEPTOR FAMILY)
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/363,745
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                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/750,134
                                                                                                                                                                                                                                                   Sequence 4, Application US/09363745 Patent No. 6194162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: CRAWFORD, ARTHUR C.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 1430
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4006
TELEFER: (703) 816-4100
INFORMATION FOR SEQ ID NO: 4:
                                                                                         TGTTCATCGACTTCCT 1087
                                                                                                                                    1249 IGCITIGIGATCICIT 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: Z2201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: single
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LENGTH: 1837 base pair
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Matches 434; Conservative
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CLASSIFICATION:
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                                                                                                                                                                                                        RESULT 10
US-09-363-745-4
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GITITIGGCACCGGAGGAAAATTIGACATTATCCAGCTGGTIGTGTACATCGGCTCAACC 1046
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APPLICANT: BUELL, GARY
TITLE OF INVENTION: P2x RECEPTORS (PURINOCEPTOR FAMILY)
UNDER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                 Score 148; DB 4; L
Pred. No. 1.6e-33;
3; Mismatches 273;
EARLIER APPLICATION NUMBER: US 09/008,185
EARLIER FILING DATE: 1998-0-1-16
EARLIER APPLICATION NUMBER: US 60/071,298
EARLIER PILING DATE: 1998-0-1-16
EARLIER APPLICATION NUMBER: US 60/071,669
EARLIER FILING DATE: 1998-0-1-16
NUMBER OF SEQ ID NOS: 32
                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 15
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                                                                                                                                                                                                                                                                                   Query Match 8.0%;
Best Local Similarity 54.9%;
Matches 361; Conservative
                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-191-136-15
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US-08-750-134A-8
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APPLICANT: About Laboratories
APPLICANT: Burgard, Beward
APPLICANT: Burgard, Beward
Burgard, Burgard, Beward
TITLE OF INVENTION: Nucleic Acids Encoding A Functional
TITLE OF INVENTION: Human Purintoreceptor P2X3 and P2X6 And Methods Of Production
TITLE OF INVENTION: And Use Thereof
TITLE OF INVENTION: And Use Thereof
TITLE OF INVENTION: And Use Thereof
CURRENT APPLICATION NUMBER: US/09/191,136B
CURRENT APPLICATION NUMBER: US/09/191,136B
EARLIER APPLICATION NUMBER: US 09/008,526
EARLIER FILING DATE: 1998-01-16
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                                                                                                                                                                                    Gaps
                                                                                                                                                                                  21;
                                                                                                                                        Length 1272;
                                                                                                                                                                                  Indels
                                                                                                                                    Score 148.4; DB 4;
Pred. No. 1.2e-33;
3; Mismatches 274;
                                                                            OTHER INFORMATION: Sequencing Primer
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GENERAL INFORMATION:
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                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                      8.0%;
                                                                                                                                                                                362; Conservative
                                                                                                                                                             Similarity
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US-09-191-136-15
LENGTH: 1272
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Matches 36
                                                            FEATURE:
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1016 TATCCAGCTGGTTGTGTACATCGGCTCAACCCTCTCCTACTTCGGTCTGGCCRCTGTGTT 1075
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    876 TCTGGGTATTAAGATCGGCTGGGTGTGCGATCTAGACAAGGCCTGGGACCAGTGCATCCC 935
                                                                                                                                                                                                                                          956 AAAAGTCTTCGGGATCCGTTTTGACATCCTGGTTTTTGGCACCGGAGGAAAATTTGACAT
                                                                                                 936 TAAATATTCCTTCACTCGCTGGATGGAGTTTCTGAGAAAGCAGTGTTTCCCCTGGCTA
                                                                                                                                                899 CAACTTCAGATACGCCAAGTACTACAA---GGAAAACAATGTTGAGAAACGGACTCTGAT
                                                 839 CAAAIACAGTITCCRICGCCTTGACGACAAGACCACCAACGIGTCCTTGIACCCTGGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P2x RECEPTORS (PURINOCEPTOR FAMILY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MG-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
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52.6%; Pred. No. 3.9e-31;
Live 3; Mismatches 376;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION WIMBER: US/09/363,745
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09363745;
Patent No. 6194162
GENERAL INFORMATION:
APPLICANT: VALERA, SOLEDAD
APPLICANT: BUELL, GARY
TITLE OF INVERVION: P2x RECEPTORS
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: 08/750,134
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: NIXON & VANDERHYE STREET: 1100 NORTH GLEBE ROAL
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NAME: CRAWFORD, ARTHUR C.
REGISTRATION NUMBER: 25,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO: 8 SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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Best Local Similarity 52.65
Matches 457; Conservative
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MEDIUM TYPE: Floppy
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STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
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                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
OPERATING SYSTEM: PC-DOS/NS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,134A
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52.6%; Pred. No. 3.9e-31;
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22-JAN-1997
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I: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
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REFERENCE/DOCKET NUMBER: 1430
TELEPHONE: (703) 816-4006
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1753 base pairs
                                                                                                                                                                                                                                                                                                                                                                                 CRAWFORD, ARTHUR C. RATION NUMBER: 25,327
                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
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Matches 457; Conservative
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STRANDEDNESS: single
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22201-4714
                                            ARLINGTON
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                                                                                              COUNTRY:
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                                                                                                                                                                        Score 140; DB 4; L
Pred. No. 3.9e-31;
5; Mismatches 340;
                                                              SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 14 LENGTH: 1421
                    us/09/191,608
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he: 103 secs
   FILE REFERENCE: 6394.US.P1
CURRENT APPLICATION NUMBER: US/C
CURRENT FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                        7.6%;
ilarity 52.3%;
Conservative
                                                                                                                        ; ORGANISM: Homo sapiens
US-09-191-608-14
                                                                                                                                                                                       Similarity
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                                                                                                              TYPE: DNA
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Best Local S
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Patent No. 6242216

CENERAL INPORMATION:
PAPLICANT: Lynch, Kevin J.
APPLICANT: Burgard, Edward C.
APPLICANT: Metzger, Randy E.
APPLICANT: Miforatos, Wende
APPLICANT: Van Biesen, T.
TITLE OF INVENTION: Nucleic Acids Encoding a Functional
TITLE OF INVENTION: Human Purinoreceptor P2XZ and P2XZ and Methods Of Production
TITLE OF INVENTION: And Use Thereof
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GGTGAAAGGCTTCGGGCGCTATGCCAACAGAGTCATGGACGTGTCGGATTATGTGACCCC 410
                              ITTGCAGGGGAACTCTTTCT---TCGTGATGACAAACTTTCTCAAAACAGGCCAAGA 370
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US-09-191-608-14
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July 18, 2003, 18:14:54 ; Search time 422 Seconds (without alignments) 9058.627 Million cell updates/sec
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7. /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Mo. Score Match Length DB ID Description 1 1846.6 99.7 1853 12 US-09-977-221-2 Sequence 2, Appli 2 1837 12.8 1389 11 US-09-983-082-1 Sequence 191, Appli 3 237 12.8 1389 11 US-09-969-125. Sequence 2.5, Appli 1 US-09-969-125. Sequence 2.5, Appli 2 147.4 8.0 2633 11 US-09-969-125. Sequence 2.5, Appli 2 147.4 8.0 2633 11 US-09-969-125. Sequence 2.5, Appli 2 15.1 US-09-977-221-3 Sequence 2.5, Appli 2 15.1 US-09-977-221-3 Sequence 2.5, Appli 2 15.1 US-09-977-221-3 Sequence 2.5, Appli 2 15.1 US-09-984-864-864-864 Sequence 31.2 Appli 2 102.6 5.5 1956 11 US-09-986-864-864-254 Sequence 102.0, Appli 2 16.5 1958 15 US-09-960-352-11220 Sequence 102.0, Appli 2 16.5 1958 15 US-09-960-352-11220 Sequence 103774, Appli 2 16.5 19.8 4.8 698 15 US-09-986-350. Sequence 5505, Appli 2 12.2 2.8 941 11 US-09-998-350 Sequence 5505, Appli 2 12.2 2.8 941 11 US-09-998-350 Sequence 250, Appli 2 12.2 2.8 941 11 US-09-916-1550 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-2154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-2154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-2154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-2154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-2154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-2154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-2154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-2154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-2154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-2154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-2154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-2154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-2154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-2154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-2154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-2154-250 Sequence 250, Appli 2 12.2 2.8 941 15 US-09-2154-250 Sequence 250, Appli 2 12.2 2

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APPLICANT: Chun, Miyoung
TITLE OF INVENTION: METHODS AND COMPOSITIONS:
TITLE OF INVENTION: CARDIOVASCULAR DISEASE 1;
FILE REFERENCE: MNI-227
CURRENT APPLICATION NUMBER: US/09/833,082
CURRENT FILING DATE: 2001-04-10

SOFTWARE: FASTSEQ for Windows Version 4.0
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16; Mismatches
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         ; ORGANISM: Homo sapiens
US-10-175-523-191
                                                            Similarity
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Matches 1830;
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Pred. No. 2.4e-53;
5; Mismatches 342;
                                                                               1057 TCGGTCTGGCCRCTGTGTTCATCGACTTCCTCATC
                                                                                                                                                                                                                                       APPLICANT: EDGET, Reinhard
TITLE OF INVENTION: Cancer Gene Determination
TITLE OF INVENTION: Cancer Gene Determination
TITLE OF INVENTION: Sets
TITLE FOR INVENTION: Sets
TITLE FOR INVENTION: Sets
CURRENT APPLICATION NUMBER: US/09/969,347
CURRENT FILING DATE: 2001-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 318
SEQ ID NO 225
LENGTH: 2633
                                                                                                                                                                                          ; Sequence 225, Application US/09969347; Patent No. US20020115085A1
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54.8%;
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US-09-969-347-225
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Best Local Similarity
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                                                                                                                                Gaps
                                                                                                                             36;
                                                                                              Score 237; DB 11; Length 1389; Pred. No. 4.8e-64;
                                                                                             Query Match 12.8%; Score 237; DB 11; Length 13
Best Local Similarity . 54.4%; Pred. No. 4.8e-64;
Matches 574; Conservative 5; Mismatches 440; Indels
                            TYPE: DNA
ORGANISM: Homo Sapiens
               LENGIH: 1389
                                                              US-09-833-082-1
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                                                                                                                                                                                                                                                                                                                                                                                                                              7.7%; Score 142.6; DB 12; Length 11270; 97.9%; Pred. No. 1.4e-33; 1.1ve 2; Mismatches 1; Indels 0; 0
                                                                                                                                                                                                                                                                                                                                  LOCATION: (5554)..(5569)
OTHER INFORMATION: This range may encompass 3 or 4 gttt repeats
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OF INTELE OF INVENTION: EROM VARIOUS CONA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 CCACGTGATCATCTTTCCTACGTTTGCTTTG 156
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 31290
     PRIOR FILING DATE: 2000-11-02
PRIOR PLIANG DATE: 2000-11-02
PRIOR FILING DAMER: GB 0108654.5
PRIOR APPLICATION NUMBER: GB 0108654.5
PRIOR TILING DATE: 2011-04-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)...(515)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 97.9
Matches 142; Conservative
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Matches 135; Conservative
                                                                                                                                                                                                                                                                                                     NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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                                                                                                                                                                                                           LENGTH: 11270
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                 SEQ ID NO.3
                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                                                                                                                                                                                                                   FEATURE:
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                                 GGCACCGGAGGAAAATTTGACATTATCCAGCTGGTTGTGTACATCGGCTCAACCCTCTCC 1052
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813 GACCGITGGTICCATCACTGCCRTCCCAAATACAGTTICCRTCGCCTTGACGACAAGACC 872
                                                                                                 873 ACCAACGIGICCIIGIACCCIGGCIACAACIICAGAIACGCCAAGIACIACAAGGAAAAC 932
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8.0%; Score 147.4; DB 12; Length 4900;
Best Local Similarity 99.3%; Pred. No. 2.6e-35;
Matches 148; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   1217 ATCTTTGGGGTGGCCACAGTTCTCTGTGACCTGCT 1251
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Sequence 3, Application US/09977221
Publication No. US20030008293A1
GENERAL INFORMATION:
TILLE OF INVENTION: CHEMICAL COMPOUNS
FILLE REFERENCE: PLS/00991/028379
CURRENT APPLICATION NUMBER: US/09/977,221
CURRENT FILING DATE: 2001-10-16
FRIOR APPLICATION NUMBER: 60/244,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MORTEN, JOHN EDWARD NORRIS, TITLE OF INVENTION: CHEMICAL COMPOUNDS FILE REFERENCE: PLS/009901/028379
CURRENT APPLICATION NUMBER: 05/09/977,221
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/244,897
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: GB 0025859.0
PRIOR APPLICATION NUMBER: GB 0026859.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09977221 Publication No. US20030008293A1 GENERAL INFORMATION:
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SEQ ID NO 1
LENGTH: 4900
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APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Magappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AN
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        988 ITITIGGCACCGGAGGAAAITIGACAITATCCAGCIGGIIGIGTACAICGGCICAACCC 1047
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APPLICANT CATER, DATIOCK
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.523
CURRENT APPLICATION NUMBER: US/09/864,864
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 94.6; DB 11;
Pred. No. 3.4e-19;
4; Mismatches 163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1048 TCTCCTACTTCGGTCTGGCCRCTGTGTTC 1076
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                                               . Sequence 254, Application US/09864864
; Patent No. US20020102679A1
                                                                                                                    APPLICANT: Xu, Jiangchun APPLICANT: Xu, Jiangchun APPLICANT: Mitcham, Jennifer L. APPLICANT: Dillon, Davin C. APPLICANT: Dodes, Michael J. APPLICANT: Lodes, Michael J. APPLICANT: APPLICANT: APPLICANT: Fling, Steve P. APPLICANT: Fling, Steve P. APPLICANT: Mannion, Jane APPLICANT: Bangon, Darrin R. APPLICANT: Bangon, Darrin R. APPLICANT: Bangon, Darrin R. APPLICANT: Bangon, Darrin R. APPLICANT: Bangon, Darrin R.
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Best Local Similarity 55.55
Matches 216; Conservative
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Pred. No. 2.5e-21;
3; Mismatches 207; Indels 15;
                                                                                                                                                                                           APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Fling, Steve P.
APPLICANT: Fling, Steve P.
APPLICANT: Mannion, Jane
APPLICANT: Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.523
NUMBER OF SEQ ID NOS: 341
SOUTHARR: OATKA INVENTION DISCLOSUITE DATABASE
SEQ ID NOS: 341
LENGTH: 1956
268 CCACGIGAICGICITIICCIAIGIIAGAIIIG 299
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                                                                                                                            Sequence 331, Application US/09864864
Patent No. US20020102679A1
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al Similarity 55.4%;
280; Conservative 3
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ORGANISM: Homo sapiens
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                                                                                                 -09-864-864-331
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                                                                                       61 AGGCACCGTGGCTCACGTCTGTAATCCCAGCGCTT 95
                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/18,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-30
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-11-33
PRIOR FILING DATE: 1999-11-33
PRIOR FILING DATE: 1999-11-33
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 103775
                                                                                                                                                                               US-10-027-632-103775
; Sequence 103775, Application US/10027632
; GENERAL INFORMATION:
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US-09-918-995-5505
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Best Local Similarity
Matches 92; Conserv
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US-10-027-632-103775
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                                                                                                                                                                                                                                                                                                                                                                                                           665 CATCACTTGTACCTTCCACAAGACTCAGAATCCACAGTGTCCCATTTTCCGACTAGGAGA 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                785 CATTGAGATCTACTGGGACTGCAACCTAGACCGTTGGTTCCATCACTGCCRTCCCAAATA 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 TICCIICCGCCGCCTAGACACCCGTGACTIGGCCCACAACGIAICCCCAGGCTACAAITI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             845 CAGTITCCRICGCCITGACGACAAGACCACCAAGTGTCCTIGTACCCTGGCTACAACTT 904
                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                      Score 90.8; DB 11; Length 276; Pred. No. 4.3e-18; 2; Mismatches 114; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 698;
                                                                                                                                                            ; OTHER INFORMATION: Clone ID: 48-LIB3058-028-Q1-K1-D8 US-09-960-352-11220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 89.8; DB 15;
Pred, No. 1.5e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          905 CAGATACGCCAAGTACTACAAGGAAAACAATGTT 938
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FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
WIMBER OF SEQ ID NOS: 15112
SEQ ID NO 11220
LENGTH: 276
                                                                                                                                                                                                                    Query Match 4.9%;
Best Local Similarity 57.7%;
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 96.8%;
Matches 92; Conservative
                                                                                                                                         ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-027-632-103774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Human
US-10-027-632-103774
                                                                                                                          TYPE: DNA
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1759 GGAAAGAGTTTCCRAAGAGTGAAGGCAGTACAGTGCTTCAAGAGTCCTTACTGAAGCC 1818 APPLICANT: Wang, David G. TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Delymorphisms in the Human Genome FILE REFERENCE: 108827.129 ; 0 Length 698; US-09-918-995-5505

Sequence 5505, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: RYOM VARIOUS CDNA LIBRARIES
FILE REPERRACE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT PILING DATE: 2001-07-30

PRIOR PILING DATE: 2001-07-30

PRIOR PILING DATE: 1999-01-20

NUMBER OF SED ID NOS: 38054

SOFTWARE: FastSEQ for Windows Version 3.0 Indels 1819 AGGCACCGIGGCICACGICIGIAAICCCACCITIT 1853 ch 4.8%; Score 89.8; DB 15; Smilarity 96.8%; Pred. No. 1.5e-17; 92; Conservative 0; Mismatches 3;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1022 GCTGGTTGTGTACATCGGCTCAACCCTCTCCTACTTCGGTCTGGCCRCTGTGTTCATCGA 1081
                                    2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 368 GTGTABARTCAGAIGCCAGCTGTACTGCCGGCTCTGCCGGCACCCACAGCBACGGAGITTC 427
                                                                                                                               113 TAAGIGGITCITCCACGIGAICATCITITCCIACG---TTTGCITTGCTCTGGIGAGIGA 169
                                                                                                                                                             170 CAAGCTGTACCAGCGGAAAGAGCCTGTCATCAGTTCTGTGCACACCAAGGTGAAGGGGAT 229
                                                                                                                                                                                                                                                                                                                                                            61
                                                                                     26 TCTGTTCGAGTACTACACGCGGCGCATCGTGCTCATCCGCAGCCGCAAAGTGGGGGCTCAT 85
                                                                                                                                                                                                                                                                                      146 AAAGGCTACCAGGAAACTGACTCCGTGGTCAGCTCCGTTACGACCAAAGTCAAGGCCT
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                                                             53 IGITITICCAGIATGAGACGAACAAGTCACTCGGATCCAGAGCATGAATTATGGCACCAT
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Patent No. US2002015092241
FIGENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: TWO ANATION:
APPLICANT: Chemault, Ruth A.
APPLICANT: Madelein Joy
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REPERROR: 210121.561
CURRENT PILING DATE: 2001-11-16
CURRENT FILING DATE: 2001-11-16
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 1742
LENGTH: 229
                                  21;
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 Length 458;
Score 57.2; DB 12; Length 4
Pred. No. 2.6e-07;
2; Mismatches 205; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             470 GACCGGAAGGTGTGTAGTRYATGAAGGG 497
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                                220; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-998-598-1742
                 Similarity
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US-09-998-598-1742
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 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 458 CAAAGGAATTCAGACCGGAAGGTGTGTRGTRYAT---GAAGGGAACCAGAAGACCTGTGA 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  515 AGTCTCTGCCTGGTGCCCCATCGAGGCAGGAGGCCCCCCGGCCTGCTCTTGAA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        684 GGTGTTCGCCTGGTGCCC---GGTGGAAGATGGGGCCTCTGTCAGCCAATTTCTGGGTAC 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             575 CAGTGCCGAAAACTTCACTGTGCTCATCAAGAACAATATCGACTTCCCCGGCCACAACTA 634
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                                                                                                                                                                                                                                                          Prior application data removed - consult PAIM or file wrapper NUMBER OF SEQ ID NOS: 2003 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 250
                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
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Pred. No. 3.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches 107;
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OTHER INFORMATION: n equals a,t,g, or
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                                                                                                          Sequence 250, Application US/09764847 Patent No. US20020132767A1
                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
LOCATION: (6)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE
LOCATION: (94)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n equals a,t,g,
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 139; Conservē
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: (112
                                                                      RESULT 15
US-09-764-847-250
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                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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BG769595 602744503
BF68946 60126481
BE38282 601267884
BE690388 602186810
BE347290 602021043
BG554327 H4027801-
BG759437 H4027801-
BG759437 H4027801-
BG769470 602742429
BE689531 uw55f09.y
AA210664 PMY0056 K
BC017458 HOme sapi
BE448796 uus muscu
BG681359 AGBNCOURT
BG70342 RC1-T1001
BG788542 AGBNCOURT
BG70342 RC1-T1001
BG788542 AGBNCOURT
AM913297 uf51604.y
AG72571 vo60e05.r
BF5899099 CMA-NN008
BH55809 CMA-NN008
BH55809 CMA-NN008
BH55207 603170249
AG45251 vo60e05.r
BG5004 wt42a02.x
AM95596 EST73776
AM975596 EST73776
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AM975596 EST73776
BM91921 AGBNCOURT
AM975596 EST384705
BM91921 AGBNCOURT
AM975506 EST384705
BM91921 AGBNCOURT
AM713768 UV85160.x
BE626188 UV85160.x
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3013)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URE: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site:
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                                                                                                                                                                                                           BC017458
BE448796
BC02099
BC681359
BI687408
BF770342
BC88542
AJ446359
AW913297
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AW975596
BM919221
BM469621
AL541451
AA713768
BE626188
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BI681932
AW899099
BI452907
AJ445426
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BI536809
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 Homo sapiens.
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TITLE
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BF347747 602022588
BG768165 602744202
BI603534 603244436
BG766449 602739207
                                                                                                                             July 18, 2003, 16:29:01; Search time 2708 Seconds (Without alignments) 11082.067 Million cell updates/sec
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                               CATCACTIGIACCITCCACAGACTCAGAATCCACAGIGICCCATTITCCGACTAGGAGA
                                                CATCTTCCGAGAAACAGGGGGATAATTTTTCAGATGKGGCAATTCAGGGCGGAATAATGGG
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                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAL plate: 12 Row: g Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4505552 This clone has the following problem: incomplete processing.
Contact:
    nisc_mgc@nbgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Shevchenko,Y., Wetherby,K.D., Bookstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffand,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,O.L., Maslello,C., Mastialo,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Plurgeon,C., Vogt,J.L., Walker,M.A.,
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                                                                                                                                                                                                                                                    /organism="homo sapiens"
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/clone="InAAGE:8628076"
/tissue_type="Brain, neuroblastoma"
/clone_lib="NHHMGC_19"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                        Score 1634.6;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                      Zhang, L.-H. and Green, E.D.
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                                                                                                                                                                                                                                                                                                                                                                                                        88.2%;
93.8%;
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Best Local Similarity 93.89
Matches 1735; Conservative
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BE347747 1000 946 bp mRNA linear EST 22-NOV-2000 602022588F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158189
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                                                                                                                                                                                                                                                                                                                                                                                                                                 539
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Homo.
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1356 CIGGCCCTCCATGACACACCCCCGATTCCTGGACAACCAGAGAGATACRGCTGCTTAGA
                           241 CIGGCCCTCCATGACACACCCCGATTACCTGGACAACCAGAGGAGATACAGCTGCTTAGA
                                                                                             1416 AAGGAGGCGACTCCTAGATCCAGGGATAGCCCYGTCTGGTGCCAGTGTGGAAGCTGCCTC
                                                                                                                                                                                           1476 CCATCTCAACTCCCTGAGRGCCACAGGTGCCTGGAGGMGCTGTGCTGCCGGAAAAAGCCG
                                                                                                                                                                                                                    360 CCATCTCAACTCCCTGAGAGCCACAGGTGCCTGGAGGAGCTGTGCTGCCGGAAAAAGGCG
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                                                                                                                                                                                                                                                                                                                                     420 GGGGCCTGCATCACCACCTCAGAGCTGTTCAGGAAGCTGGTCCTGTCCAGACACGTCCTG
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 946)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NCI_CGAP_Brn67"
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/db_xref="taxon:9606"
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BF347747
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TITLE
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BF347747
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                                            1672 CCGCTGGAGGATCCGGAAAGAGTTTCCGAAGAGTGAAGGGCAGTACAGTGGCTTCAAGAG 1731
                   1745 CCGCTGGAGGATCCGGAAAGAGTTTCCRAAGAGTGAAGGGCAGTACAGTGGCTTCAAGAG 1804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TACAGGAAGAAGTGCGAGTCCATTGTGGAGCCAAAGCCGACATTAAAGTATGTGTCTTTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov
Tissue Procurement: DCID/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12018 row: k column: 22
High quality sequence stop: 772.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 795)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: breast, Vector: pcMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally; oligo-dr primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 GIGGAIGAAICCCACATIAGGAIGGIGAACCAGCAGCIACIAGGGAGAGAGICTGCAAGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1116 CGCTCCCATATTTATCCCTGGTGCAAGTGCTGTCAGCCCTGTGTGGTCAACGAATACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1176 TACAGGAAGAAGTGCGAGTCCATTGTGGAGCCGAAAAGCCGACATTAAAGTATGTGTCCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIT-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/lab_host="DH10B (phage-resistant)"
                                                                                                                                            1732 TCCTTACTGAAGCCAGGCACCGTGGCTCACGTCTGTAATCCCAGCGCTT 1780
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                                                                                                                 1805 ICCTTACTGAAGCCAGGCACCGTGGCTCACGTCTGTAATCCCACCTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="NIH_MGC_87"
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97.7%;
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BI861622
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BI861622
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SOURCE
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49 CGCAGGGAGGCAGGCTGTCACCATGCCGGCCTGCAGCTGCAGTGATGTTTTCAGTA 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 CTACACCTTCCCTTTTGCAGGGAACTCTTTCTTCGTGATGACAACTTTCTCAAAACAG 408
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                                                                              Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 TGAGACGAACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAGTGGTTTTT
                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostom Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo, I hases 1 to 937)

11 H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 CGCAGGGAGGCTGTCACCATGCCGGCCTGCTGCAGCTGCAGTGATTTTCCAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 AGGAGATCGYGGAGAATGGA--GTGAAGAAGTTGGTGCACAGTGTCTTTGACACCGCAGA
                                                                                                                                                                                                          CDNA Library Preparation. Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 666.8; DB 12; Length 937;
Pred. No. 6.2e-169;
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                                                                                                                                                                                                                                                                                                  Plate: LLCM1761 row: d column: 02
                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:4877137"
/clone_lib="NIH_MGC_49"
                                                                                                                                                                                                                                                                                                                High quality sequence stop: 801.
Location/Qualifiers
                    GI:14078818
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90.5%;
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                                                                Homo sapiens
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COMMENT
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                                                                                                                                                                  64
                                                                                                                                                                                            17
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert Size 2:3 kb. Constructed by Life Pechnologies. Note: this is a NCL_CGAP Library." 254 c 251 g 204 t
                                                                                                                                                                              CCACGIGATCATCITTCCTACGITTGCTTTGCTCTGGGGAGTGACAGCTGTACCAGGG
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                                                                                                                                     Gaps
                                                                                                                                     10;
                                                                                                       946;
                                                                                                         Length
                                                                                                                                     31; Indels
                                                                                                   Score 671.8; DB 12
Pred. No. 2.8e-170;
4; Mismatches 31;
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BG766449 769 bp mRNA linear EST 15-MAY-2001 602739207F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4869288 5', mRNA sequence.
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                                                                                                                                                                                                                                                                 72
size-selected for average insert size 2.3 kb and normalized to RoT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAGACGAACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAGTGGTTCTT
                                                                                                                                                                                                                                                                                                                      TGAGACGAACAAAGTCACTCGGATCCAGAGCATGATTATGGCACCATTAAGTGGTTCTT
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                                                                                                                                                                                                 Gaps
                                                                                                                                                                                               <u>.</u>
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                                                                                                                                                           Score 645.4; DB 13; Length 932; Pred. No. 3.8e-163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           829 GAATATGGGCATTGAAATTACCTGGGACTGGCACCTAGAACGTGGTTCCATCAATGTACA 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRL), Shiraki
Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov. g column: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 932)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unbublished (1999)
                                                                                                                                                                                                                                             CAGTGGAAGAGGCCCCCCGGCCTGCTCTTGAACAGTGCCGAAAACTTCACTGTGCTCA
                                                                                                                                                                                                                           TCAAGAACAA-TATCGACTTCCCCGGCCACAACTACACCACGAG-AAACATCCTGCCAGG
                                                                                                                                                                                                                                                                                                TITAAACAICACTIGIACCTICCACAAGACICCAGAAICCACAGIGICCCATTTTCCG-AC
                                                                                                                                                                                                                                                                                                                                                                  TAGGAGA-CATCTTCCGAGAAACA-GGCGATAATTTTTCAGATGKGGCAATTCAGGGCGG
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                                                                                                                                                                           ACCGAGGTTGTAAAAAGGGATGGATGGACCCCCAGAGCAAAGGAATTCAGACCGGAAGGT
                                                                                   GTGTAGTRYATGAAGGGAACCAGAAGACCTGTGAAGTCTCTGCCTGGTGCCCCATCGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCCAAATACAGTTTCCRTCGCCTTGACGACAAGAC 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: LLAM11725 row: g column: 09
High quality sequence stop: 747.
Location/Qualifiers
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/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
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/nore="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI, Site_2: Sall-XhOI (gtcgap ); Oligo-dr primed using primer 5'-TTTTTTTTTTTTTTTTTTVTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI598073 860 bp mRNA linear EST 07-SEP-2001
603252308F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5304048 5',
                                                                                                                                                        721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Micheal J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninoid (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Libra at:
543 GIGGAAGAGGCCCCCCGGCCTGCTCTTGAACAGTGCCGAAAACTTCACTGTGCTCATC 602
                                                                                                                                                                                                             603 AAGAACAATATCGACTTCCCCGGCCACAACTACCACGAGAAACATCCTGCCAGGTTTA 662
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Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
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Location/Qualifiers
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/db_xref="taxon:9606"
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Mammalia; Eutheria; P.
1 (bases 1 to 860)
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                                                      Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 769) MIH-WGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can life out through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov column: 01
Plate: LLCMIAG row: m column: 01
High quality sequence stop: 654.
Location/Qualifiers
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Pred. No. 2.8e-156;
3; Mismatches 25;
                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Cgapbs-rémail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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/db_xref="taxon:9606"
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95.2%;
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Pred. No. 2.1e-138;
3; Mismatches 50;
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                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
      column:
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High quality sequence stop: 601.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 841)
                                                      CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at: http://image.llnl.gov
                                                                                                                                              GAAAGAGCCTGTCATCAGTTCTGTGCACACGTGAAGGGGGATAGCAGAGGGTGAAAGA
                                                                                                                                                                                                                                                                                                      CACCTTCCCTTTCCAGGGGAACTCTTTCTTCGTGATGACAAACTTTCTCAAAACAGG
                                                                                                                                                                                                                                                                                                                      CCAAGAGCAGCGGTTGTCCCCGAGTATCCCACCCGCAGGACGCTCTGTTCCTCTGACCG
                                                                                                                                                                                                                                                                                                                                                                                                          AGGTTGTAAAA-AGGGATGGATGGACCCGCAGAGCAAAGGAATTCAGACCGGAAGGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Rotacts Trausberg, Ph.D.
Emall: ogapbs-rémail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                        CGCAGGGAGGGAGGCTGTCACCATGCCGGCCTGCTGCAGCTGCAGTGTTTTCCAGTA
                                                                                         65 TGAGACGAACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAGTGGTTCTT
                                                                                                                                                                                                GAAAGAGCCTGTCATCAGTTCTGTGCACCAAGGTGAAGGGGGATAGCAGAGGTGAAAGA
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                 Indels
              18;
 Pred. No. 3.6e-141;
                3; Mismatches
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 95.9%;
              629; Conservative
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BG769595
Best Local Similarity
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B17 bp mRNA linear EST 21-JUL-2000 601297884F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628076 5', mRNA sequence.
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GTAGTRYATGAAGGGAACCAGAAGACCTGTGAAGTCTCTGCCTGGTGCCCCCATCGAGGCA 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 CCAAGAGCA--GCGGTTGTGTCCCGAGTATCCCACCCGCAGGACGCTCTGTTCCTCTGAC 422
                                                                                                                                                                        423 CGAGGTTCTAAAAAGGGATGGATGGACCCCGCAGAGCAAAGGAATTCAGACCGGAAGGTGT 482
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 817)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
flound through the I.M.A.G.E. Consortium/Link at: image.llnl.gov
Flour LLCM312 row: g column: 21
High quality sequence stop: 646.
                                                                                                                                                                                                                                                                                                                                                                                               543 GIGGAAGAGCCCCCCGGCCIGCICIIGAAC-AGIGCCGAAAACIICACIGIGCICAI
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                                                                                                                                                                                                                                                NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
Unpublished (1999)
Contact: Rotasberg, Ph.D.
Email: ogapbs-refactail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAACATCACTTGTACCTTCCACAAGACTCCAGAATCCACAGTGTCCCATT 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3628076"
/clone_lib="NIH_MGC_19"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 908)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ogaphs-remail.nih.gov
Tissue Procurement: ArCC/DCTD/DTP
Tissue Procurement: ArCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LiNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Linn at:
http://incythe I.M.A.G.E. column: 04
High quality sequence stop: 668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 TGAGACGAACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAGTGGGTCCTT
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                            CGACTAGGAGACATCTTCCGAGAAACAGGCGATAATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                               BF689446.1 GI:11974854
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al Similarity 92.9%;
659; Conservative
                                                                                                                                                                                             mRNA sequence.
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Best Local Si
Matches 659;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GMGCTGTGCTGCCGGAAAAAGCCGGGGGCCTGCATCACCACCTCAGAGCTGTTCAGGAAG 1571
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                                                                                     In (Masses 1.0.1022)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Luppublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: ogapbs-remail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CONA Library Preparation: Ling Hong/Rubin Laboratory

CONA Library Preparation: Ling Hong/Rubin Laboratory

CONA Library Paraged by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCMLISS row: c column: 04

High quality sequence start: 11

High quality sequence start: 11

High quality sequence stop: 688.
                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGCTGTGCTGCCGGAAAAAGCCGGGGGCCTGCATCACCACCTCAGAGCTGTTCAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      475 CTGGTCCTGTCCAGACACGTCCTGCAGTTCCTCCTGCTCTACCAGGAGCCCTTGCTGGCG
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                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1022)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1022;
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Pred. No. 1.8e-120;
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                                    Homo sapiens
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                                                                                                                                                                                                                                                            TGATCAICITTICCTACGITTGCTTTGCTCTGGTGAGTGACAAGCTGTACCAGCGGAAAG 189
                                                                                                                                                                                                                                                                                                                                                                                TCGYGGAGAATGGAGTGAAGATGGTGCTACAGTGTCTT-TGACACCGCAGACTACACC 308
                                                                                                                                                                                                                                                                                                                                                                                                 GAGCAGCGGTTGTGTCCCGAGTATCCCACCCG--CAGGACGCTCTGTTCCTCTGACCGAG 426
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(Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." 199~c~216~g~188~t
                                                                                                                                                                                                                TCTTCCGAGAAACAGGCGATAATTTTTCAGATGKGGCAATTCAGGGCGGAATAATGGGCA
                                                                                                                                      GGAGGGAGGCTGTCACCATGCCGGCCTGCTGCAGCTGCAGTGATGTTTCCAGTATGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCCCTTTGCAGGGGAACTCTTTCTTCGTGATGACAAACTTTCTCAAAACAGAAGGCCAA
                                                                                                           Gaps
                                                                                                         102;
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                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424 GTTGTAAAAAGGGATGGACCCGCAGAGCAA------
                                                                                                        47;
                                                                                        1.7e-123;
                                                                                        Pred. No. 1.7e
3; Mismatches
                                                                          Score 498.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
BF690388
BF690388.1 GI:11975796
                                                                          Query Match 26.9%;
Best Local Similarity 81.7%;
Matches 677; Conservative
                              214 a
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BF690388/c
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#4027B01-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone BQ554327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         National Institute on Aging/National Institutes of Health National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA-Fmall: odnaelganu.grc.nia.nih.gov.
This clone set shas been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details. Plate: H4027 row: E column: 01
Seq primer: -21M13 Reverse
High quality sequence stop: 642
POLTA=No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1302 GGCCAAGAAGTCCSAAGACCTGYGATGGACTTCACAGATTTGTCCAGGCTGCCCCTGGCC 1361
                                                                                           288 GGAGATCGTGGAGAATGGAGTGAAGAGTTGGTGCACAGTGTC-TTGACACCGCAGACTA 346
                                                                     305 CACCTTCCCTTTGCAGGGGAACTCTTTCTTCGTGATGACAAACTTTCTCAAAACAGAAGG 364
                                                                                                                                                                365 CCAAGAGCAGCGGTTGTGTCCCGAGTATCCCACCGCAGGACGCTCTGTTCCTCTGACCG 424
                                                                                                                                                                                                            406 CCAAGAGCAGCGGTTGTGTCTCCCGAGTATCCCACCGCAGGACGCTCTGTTCCTCTGACCG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 642)
VanBuren,V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G., Martin,P.R., Stagg,C.A., Bassey,U., Aiba,K., Hamatani,T., Kargul,G.J., Luo,A.G. and Ko,M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assembly, verification, and initial annotation of NIA 7.4K mouse cDNA clone set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGCCGCACATTCGCATGGTGGACCAGCAGCAGCTGCTTGGGAAAAGTCTGCAAGTTGTGAAA
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; clone is among a rearrayed set of 7,407 clones from than 20 cDNA libraries."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.6%; Score 400.8; DB 14; Length 642; 80.2%; Pred. No. 4.1e-97; ive 4; Mismatches 111; Indels 0;
                                                                                                                                                                                                                                                           425 AGGITGTAAAAAGGGAIGGAIGGACCCCCAGAGCAAAGGAAITCAGAC 472
                                                                                                                                                                                                                                                                                                     513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="H4027E01"
/clone_lib="NIA Mouse 7.4K cDNA Clone Set"
/sex="mixed"
                                                                                                                                                                                                                                                                                      466 AGGTTGTAAAAAGGGATGGATGGACCCGCAGAGCAAAGGAATTCAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="niaEST: H4027E01-5"
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    .642
/organism="Mus musculus"
/strain="C57BL/6"

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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ554327.1 GI:21455215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2002)
Other_ESTs: H4027E01-3
Contact: Yong Qian
Laboratory of Genetics
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Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Buteleostomi,
Mammalla; Butheria; Primates; Catarrhini; Hominidae, Homo.

1 (bases 1 to 543)

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammallan Gene Collection (MCC)

AL Ompublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabe-rémail.inh.gov

Tissue Procurement: David N. Louis, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Genomics, Inc.

CLORA Library Preparation: Life Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

http://image.llnl.gov f column: 12

High quality sequence stop: 543.

Location/Qualifiers
                                                                                                                                                                                                                                                        BF347290 543 bp mRNA linear EST 22-NOV-2000 602021043F1 NCI_CGAP_Brn67 Homo sapiens CDNA clone IMAGE:4156427
1752 AGGATCCGGAAAGAGTTTCCRAAGAGTGAAGGGCAGTACAGTGCCTTCAAGAGTCCTTAC 1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 CGCAGGGAGGCAGGCTGTCACCATGCCGGCCTGCAGCTGATGTTTCCAGTA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 TGAGACGAACAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAGTGGTTCTT 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 GGAGATCGYGGAGAATGGAGTGAAGAAGTTGGTGCACAGTGTCTTTGACACCGCAGACTA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 CGCAGGGAGGGAGGCTGTCACCATGCCGGCCTGCTGCAGCTGCAGTGTTTTCCAGTA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site=2: SA11; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="line"NCI_CGAP_Brn67"
/tissue_type="anaplastic oligodendroglioma with lp/199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 4.7e-105;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                  5', mRNA sequence.
BF347290
BF347290.1 GI:11294885
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al Similarity 98.9%;
463; Conservative
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GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-CNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                          cecaegeaegeaegerercaccareccegecrecrecrecrecrecrecrerrrrrccaera 108
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
  into EcoRI/XhoI sites using the following 5' adaptor:
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ogapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                       Length 783;
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Pred. No. 3.3e-94;
3; Mismatches 16
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                                                                                                                                         213 g
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BF347097.1 GI:11294692
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/lab_host="DB10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: Xho!; Site_2:
ECORI; cDNA made by oligo-dr priming. Directionally cloned
                                                            1421
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                                                                                                                                                                                                                        CAACTCCCTGAGRGCCACAGGTGCCTGGAGGMGCTGTGCTGCCGGAAAAAGCCGGGGGCC 1541
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                                                                                                                                         GCGACTCCTAGATCCAGGGATAGCCCYGTCTGGTGCCAGTGTGGGAAGCTGCCTCCCATCT 1481
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301. #GCATCACCCCCCAAGCTCTTCCATAAGCTCGTGCTGTCCCGAGACACCCTGCAGCTC 360
                                                                                                                                                                                                                                                                                                                                                                                                         481 TITGCCATTCTGCCCAGCTGTTGCCGCTGGAGGATCCGGAAGGAGTTCCCCAAGACCGAG 540
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1 (bases 1 to 783)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Ling Hong/Rubin Laboratory DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) BNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                        CTCCATGACACCCCCGATTCCTGGACAACCAGAGAGATACRGCTGCTTAGAAAGGAG
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Plate: LLCM1748 row: i column: 07
High quality sequence stop: 555.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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/clone_lib="NIH_MGC_49"
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://image.llu.gov
Plate: LLAM9429 row: g column: 13
High quality sequence start: 39
High quality sequence stop: 541.
Location/Qualifiers
I. 555
Corganism="Homo sapiens"
(Ab_xref="Hixon:9606"
/clone="IRAGE:415452"
/clone="IRAGE:415452"
/clone="IRAGE:415452"
/clone="IRAGE:415452"
/clone="IRAGE:415452"
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/clone="IRAGE:415452"
/clone="Lib="NCI_CGAP_BEIN67"
/clone="Lib="NCI_CGAP_BEIN67"
/clone="Lib="Mortage and partic oligodendroglioma with lp/19q"
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                                                                                                                                                                                                                                                                                          /lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Search completed: July 18, 2003, 19:00:05 Job time: 2721 secs